

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 18:05:14 ; Search time 173 Seconds
(without alignment)
2604.485 Million cell updates/sec

Title: US-09-834-792D-4
Perfect score: 6093
Sequence: 1 MQDVQGRPGSGDAEDRE.....HRGLDQWEGCAGQPPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6093	100.0	1165	4	AAB86162 Human MTR
2	6093	100.0	1165	5	AAM51708 Human TRP
3	6093	100.0	1165	5	AB83855 Human ltr
4	6093	100.0	1165	7	ADJ69344 Human hea
5	6093	100.0	1165	8	ADR48686 Transient
6	6078	99.8	1167	8	ADR87161 Human bet
7	6034	99.0	1179	4	AAB86165 Human MTR
8	5088.5	83.5	1158	4	AAB86164 Mouse MTR
9	5088.5	83.5	1158	5	AB83854 Mouse ltr
10	5088.5	83.5	1158	8	ADR87163 Mouse bet
11	5080.5	83.4	1158	4	AAB86166 Mouse MTR
12	5073	83.3	1157	5	AAM51707 Mouse TRP
13	5025.5	82.5	1156	8	ADR87165 Rat betat
14	5008.5	82.2	1164	5	AB83853 Rat L-TRP
15	4534	74.4	872	4	AAB86163 Human MTR
16	2448.5	40.2	1166	5	ABG61907 Prostate
17	2448.5	40.2	1166	7	ADN39240 Cancer/an
18	2448.5	40.2	1166	7	ADN39598 Cancer/an
19	2448.5	40.2	1214	3	AAY95436 Human cal
20	2448.5	40.2	1214	7	ADH62712 Ca activa
21	2448.5	40.2	1214	8	ADR73512 Human TRP
22	2448.5	40.2	1214	8	ADSI2775 Transient
23	2444.5	40.1	1214	5	AAE20283 Human Trp
24	2428	39.8	1127	8	ADL06543 Human tum
25	2412.5	39.6	1129	4	AAB85974 Human TLC

ALIGNMENTS

RESULT 1

AAB86162
ID AAB86162 standard; protein; 1165 AA.

AC AAB86162;

DT 09-AUG-2001 (first entry)

DE Human MTR1 protein containing exon 18 fragment.

KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
KW 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;
KW cell growth; cell death; cell differentiation; urogenital disease;
KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
KW rhabdomyosarcoma.

OS Homo sapiens.

PN WO200132693-A2.

XX 10-MAY-2001.

XX 06-NOV-2000; 2000WO-DE003876.

XX 04-NOV-1999; 99DE-01053167.

XX (UYGU-) UNIV GUTENBERG JOHANNES.

XX Prawitt D, Pelletier J, Zabel B;

XX WPI; 2001-316417/33.

XX N-PSDB; AAH20574.

XX DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann syndrome and tumors, also related proteins and antibodies.

XX Claim 10; Fig 4; 46pp; German.

XX This invention describes a novel DNA sequence (I) encoding the MTR1 protein that: (i) has at least one biological activity of a TRP (transient receptor potential) family protein; (ii) is connected with etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the invention have anticancer and developmental activity. MTR1 is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis

Adh51623 Human 186
Adr65995 Human pro
Adr66893 Human pro
Abg72088 Human tra
Aa82018 Human sec
Adsl2777 Transient
Asg61852 Prostate
Adsl2779 Human TRP
Abm84440 Human dia
Adr43185 Human REM
Aay92944 Human TRP
Aay95439 Human cal
Ab36865 Human put
Abb76459 Human lon
Abb84544 Human tra
Adc47022 Human LTR
Adc77685 Human 222
Adc83633 LTRPC3-re
Adq89102 Human uro
Adc47034 Mouse LTR

CC and cell growth, death and differentiation, and in urogenital diseases,
 CC including polycystic kidney disease. (I) and related ribozymes, antisense
 CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
 CC associated with altered expression of the MTR1 gene or activity of its
 CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
 CC thalidomide tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
 CC used for diagnosis of such diseases. (I) can also be used for recombinant
 CC production of MTR1 proteins (II) (used for analysis, characterization and
 CC therapy), as tissue or chromosomal markers, for identifying genetic
 CC diseases and related sequences, as primers for genetic fingerprinting, as
 CC source of oligonucleotides for biochips, and to raise anti-protein or
 CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
 CC competitive assays for (II), as tissue markers, for identifying
 CC interacting proteins and in screening for (ant)agonists. This sequence
 CC represents a human MTR1 protein described in the method of the invention
 XX
 SQ Sequence 1165 AA;

Query Match 100.0%; Score 6093; DB 4; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVQGPGRGSGDADRELGHRGEVNFPGSGKRGKFRVVPVSGVAPSVLFDLLAEW 60
 DB 1 MDVQGPGRGSGDADRELGHRGEVNFPGSGKRGKFRVVPVSGVAPSVLFDLLAEW 60
 QY 61 HLPAPNLVSVLGEQEPFAMKSWLADVLKGLVKAQSTGAWILTSALRVGLRHVGQAV 120
 DB 61 HLPAPNLVSVLGEQEPFAMKSWLADVLKGLVKAQSTGAWILTSALRVGLRHVGQAV 120
 QY 121 RHSLASTSTKVRVAVGASLGRVLRRLLEAEQEDFPVHPEDDGGSGPLCSLDSNL 180
 DB 121 RHSLASTSTKVRVAVGASLGRVLRRLLEAEQEDFPVHPEDDGGSGPLCSLDSNL 180
 QY 181 SHFIIVEPGPGGGLTELRLEKHSIQEAGYGGTGSIEIPVLCVLLVNGDNTLRI 240
 DB 181 SHFIIVEPGPGGGLTELRLEKHSIQEAGYGGTGSIEIPVLCVLLVNGDNTLRI 240
 QY 241 SRAVEQAAFWLILVSGGIGADVLAAVLPKVAEKQFKEKFPKSHFSDIVRWT 300
 DB 241 SRAVEQAAFWLILVSGGIGADVLAAVLPKVAEKQFKEKFPKSHFSDIVRWT 300
 QY 301 KLLQNTSHOHLITVDFEQRGSELDTVILKALVACKSHSQBPQDYDLKLAVADR 360
 DB 301 KLLQNTSHOHLITVDFEQRGSELDTVILKALVACKSHSQBPQDYDLKLAVADR 360
 QY 361 VDIKSEIFNGDVEWKSCLBEVMDVLSVKNPFRVLFVNDGADVADFLTYGRLOELR 420
 DB 361 VDIKSEIFNGDVEWKSCLBEVMDVLSVKNPFRVLFVNDGADVADFLTYGRLOELR 420
 QY 421 SVSRKSLFDLLQKQEARLTLAGLGTQQAEPAPFSLHEVSRVLKDFLQDACRG 480
 DB 421 SVSRKSLFDLLQKQEARLTLAGLGTQQAEPAPFSLHEVSRVLKDFLQDACRG 480
 QY 481 FYQDGRPDARRAEKPAKPTGOKWLLDNKSENPRDLFLWAVLQNRHEMATYFWAM 540
 DB 481 FYQDGRPDARRAEKPAKPTGOKWLLDNKSENPRDLFLWAVLQNRHEMATYFWAM 540
 QY 541 QOEGVAALAAACKILKEMSHLETEAEARAAREAKYERLALDLFSECVSNSEARAFALLV 600
 DB 541 QOEGVAALAAACKILKEMSHLETEAEARAAREAKYERLALDLFSECVSNSEARAFALLV 600
 QY 601 RNRCSKTTCLHLATEADAKAFPAHDGQVAFTRIWWGMAAGTPIRLLLGAPLCPALV 660
 DB 601 RNRCSKTTCLHLATEADAKAFPAHDGQVAFTRIWWGMAAGTPIRLLLGAPLCPALV 660
 QY 661 YTNLITFSEAPLRTGLDQLDLSLDTSEKSPVGLQSRVEELVEAPRAQDGRPAVFL 720
 DB 661 YTNLITFSEAPLRTGLDQLDLSLDTSEKSPVGLQSRVEELVEAPRAQDGRPAVFL 720
 QY 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQSGPSEVLYFWVFTVL 780
 DB 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQSGPSEVLYFWVFTVL 780

QY 781 BEIRQGFPTDTHLVKKFTLYVGDNNKNCMDVAIFLPIVGVTCRMLPSAFEAGRTVLAM 840
 DB 781 BEIRQGFPTDTHLVKKFTLYVGDNNKNCMDVAIFLPIVGVTCRMLPSAFEAGRTVLAM 840
 QY 841 DPMVFTLRLIHFIAHKLQGLPKIIVVERMKDVFFLFFLSVMLVAYGVTTQALLHPHDG 900
 DB 841 DPMVFTLRLIHFIAHKLQGLPKIIVVERMKDVFFLFFLSVMLVAYGVTTQALLHPHDG 900
 QY 901 RLEWIFRVLRYPLQIFQIPDEIDAEARVNCSTHPLLEDSPSCPSLYANMLVILLV 960
 DB 901 RLEWIFRVLRYPLQIFQIPDEIDAEARVNCSTHPLLEDSPSCPSLYANMLVILLV 960
 QY 961 TFLVTVNLLNLLIAMFSTYFQVQGNADFMKFRQYNLIVEYHERPALAPPFILLSHL 1020
 DB 961 TFLVTVNLLNLLIAMFSTYFQVQGNADFMKFRQYNLIVEYHERPALAPPFILLSHL 1020
 QY 1021 SLTLRRVPKKEAEHREHLERDLPDLQKVVTVETVQKENFLSKMKRRDRSEGEVLRK 1080
 DB 1021 SLTLRRVPKKEAEHREHLERDLPDLQKVVTVETVQKENFLSKMKRRDRSEGEVLRK 1080
 QY 1081 TAHRVDFIAKYLGGELREQEKRICKLESQINYCSVLVSSVADVLAQGGGPRSSQHCGBGSQ 1140
 DB 1081 TAHRVDFIAKYLGGELREQEKRICKLESQINYCSVLVSSVADVLAQGGGPRSSQHCGBGSQ 1140
 QY 1141 LVAADHRGGLDGEWQPGAGQPPSDT 1165
 DB 1141 LVAADHRGGLDGEWQPGAGQPPSDT 1165
 RESULT 2
 AAMS1708
 ID AAMS1708 standard; protein; 1165 AA.
 XX
 AC AAMS1708;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Human TRP8.
 XX
 KW Mouse; human; TRP8; transient receptor potential channel;
 KW taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;
 KW pharmaceutical.
 XX
 OS Homo sapiens.
 XX
 DN WO200179448-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US012608.
 XX
 PR 17-APR-2000; 2000US-0197491P.
 PR 13-APR-2001; 2001US-00834792.
 XX
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 XX
 PI Margolskee RF, Huang L, Rong M, Max M, Perez CA;
 XX
 DR WPI; 2002-017608/02.
 DR N-PSDB; AA199708.
 XX
 PT A new transient receptor potential channel, designated TRP8, is expressed
 PT in taste receptor cells and associated with perception of bitter and
 PT sweet taste, and is useful to find new flavor enhancers.
 XX
 PS Claim 9; Fig 4; 55pp; English.
 XX
 CC The invention relates to a mouse and human transient receptor potential
 CC channel, TRP8, expressed in taste receptor cells and associated with the
 CC perception of bitter and sweet taste. Modulators of TRP8 are useful as
 CC flavour enhancers in foods, beverages and pharmaceuticals

SQ	Sequence 1165 AA;	
Query Match	100.0%; Score 6093; DB 5; Length 1165;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1165; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MDVQGPSPGDAEDRRELGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFDLLLAEW 60	
DB	1 MDVQGPSPGDAEDRRELGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFDLLLAEW 60	
QY	61 HLPAPNLVYSLVGBEOPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRVLARHVGOAV 120	
DB	61 HLPAPNLVYSLVGBEOPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRVLARHVGOAV 120	
QY	121 RDHSLASTSKVRVAVGASLGRVILHRIIEEAQEDFPVHYPPDDGSGQPLCLSDSNL 180	
DB	121 RDHSLASTSKVRVAVGASLGRVILHRIIEEAQEDFPVHYPPDDGSGQPLCLSDSNL 180	
QY	181 SHFILVEPPGPKGDLTELRLRLEKHISEORAGYGGTGSIEIPVLCLLVNGDPNLTLEI 240	
DB	181 SHFILVEPPGPKGDLTELRLRLEKHISEORAGYGGTGSIEIPVLCLLVNGDPNLTLEI 240	
QY	241 SRAVEQAAPWLILVSGGGIADVLAALVNQPHLLVPKVAEKQFKEKFPKSHFSEWIDIVRT 300	
DB	241 SRAVEQAAPWLILVSGGGIADVLAALVNQPHLLVPKVAEKQFKEKFPKSHFSEWIDIVRT 300	
QY	301 KLLQNTSHOHLITVDFEQQSGSELDVILKALVKACKSHSOEPQDYLDLKLAVADR 360	
DB	301 KLLQNTSHOHLITVDFEQQSGSELDVILKALVKACKSHSOEPQDYLDLKLAVADR 360	
QY	361 VDIKSEIFNGDVEWKSCLBEVMDALVSNKPEFVRLFDVNGADVDFLTVGRLOELYR 420	
DB	361 VDIKSEIFNGDVEWKSCLBEVMDALVSNKPEFVRLFDVNGADVDFLTVGRLOELYR 420	
QY	421 SVSRKSLFLDLQKQEARLTLAGLGTQQAEPAPFSLHVSRLVKDFLODACRG 480	
DB	421 SVSRKSLFLDLQKQEARLTLAGLGTQQAEPAPFSLHVSRLVKDFLODACRG 480	
QY	481 FYQDGRPGDRAEKGPAKPTGQKWLIDLQKSENPRWDLFLWAVLQNRHEMATYFWAM 540	
DB	481 FYQDGRPGDRAEKGPAKPTGQKWLIDLQKSENPRWDLFLWAVLQNRHEMATYFWAM 540	
QY	541 GQGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECVSNSEARAFALLV 600	
DB	541 GQGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECVSNSEARAFALLV 600	
QY	601 RNRCSKTTCLHLATEADAKAFFAHDGVQAFILTRIWWGDMAGTPIRLLAGAFLCPALV 660	
DB	601 RNRCSKTTCLHLATEADAKAFFAHDGVQAFILTRIWWGDMAGTPIRLLAGAFLCPALV 660	
QY	661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPILYGLQSRVEELVEAPRAQGRGPRAVFL 720	
DB	661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPILYGLQSRVEELVEAPRAQGRGPRAVFL 720	
QY	721 LTRWRKFWCAPVTFLGNVVMYFAFLFTFYLLVDPRPPQPGSPGPEVTLFWFVTLVL 780	
DB	721 LTRWRKFWCAPVTFLGNVVMYFAFLFTFYLLVDPRPPQPGSPGPEVTLFWFVTLVL 780	
QY	781 EIRIQGFPTDEDTHLVKKFTLYVGDNNKCDMVAIFLFIQVTCRMLPSAFAGRTVLAM 840	
DB	781 EIRIQGFPTDEDTHLVKKFTLYVGDNNKCDMVAIFLFIQVTCRMLPSAFAGRTVLAM 840	
QY	841 DMVFTLRLIHIFAIHQGLPKIIVVERMMKVFFFLFPLSVLVAIVGTQTALLPHDG 900	
DB	841 DMVFTLRLIHIFAIHQGLPKIIVVERMMKVFFFLFPLSVLVAIVGTQTALLPHDG 900	
QY	901 RLEWIFRRVLYRYLQIFGQIPLEIDEARVNCSTHPLLEDSPSCPSLYANWLIVILLV 960	
DB	901 RLEWIFRRVLYRYLQIFGQIPLEIDEARVNCSTHPLLEDSPSCPSLYANWLIVILLV 960	
QY	961 TFLLVNTVNLMLNLIAMFSYTFVQVQGNADMFWKFORYNLIVEYHERPALAPPFILLSHL 1020	
DB	961 TFLLVNTVNLMLNLIAMFSYTFVQVQGNADMFWKFORYNLIVEYHERPALAPPFILLSHL 1020	

QY	1021 SLTLRRVFKKEABHKREHLERDLDPDLQKQVVTWETVOKENFLSKMEKRRDRDSEGEVLRK 1080	
DB	1021 SLTLRRVFKKEABHKREHLERDLDPDLQKQVVTWETVOKENFLSKMEKRRDRDSEGEVLRK 1080	
QY	1081 TAHRVDFIAKVLGGLREQEKRICKLESQINVCYSLVSSVADVLAQGGGPRSSQHCGECSQ 1140	
DB	1081 TAHRVDFIAKVLGGLREQEKRICKLESQINVCYSLVSSVADVLAQGGGPRSSQHCGECSQ 1140	
QY	1141 LVAADHRGGLDGWEOPGAGOPPSTD 1165	
DB	1141 LVAADHRGGLDGWEOPGAGOPPSTD 1165	
RESULT 3		
ABB83855		
ID	ABB83855 standard; protein; 1165 AA.	
XX		
AC	ABB83855;	
XX		
DT	30-SEP-2002 (first entry)	
XX		
DE	Human ltrpc6 SEQ ID NO 8.	
XX		
KW	Human; ltrpc6; taste; cell signalling; TC-ICS; food; pharmaceutical;	
KW	taste cell-specific ion channel subunit.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200254069-A1.	
XX		
PD	11-JUL-2002.	
XX		
PF	26-DEC-2001; 2001WO-US049808.	
XX		
PR	29-DEC-2000; 2000US-0259379P.	
PR	21-DEC-2001; 2001US-00026188.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Zuker CS, Zhang Y;	
XX		
DR	WPI; 2002-583632/62.	
XX	N-PSDB; A8N85736.	
PT	Identifying modulators of taste signaling in taste cells for use in food	
PT	and pharmaceutical industries to customize and regulate taste, by	
PT	determining effect of the compound on a taste cell-specific ion channel	
PT	subunit.	
XX		
PS	Claim 1; Page 305; 306pp; English.	
XX		
CC	The invention relates to identifying (M1) a compound that modulates taste	
CC	signalling in taste cells, by contacting the compound with a eukaryotic	
CC	host cell or cell membrane which expresses a taste cell-specific ion	
CC	channel subunit (TC-ICS), and determining a functional effect of the	
CC	compound upon a transmembrane ion flux of a predetermined ion,	
CC	identifying a compound that modulates taste signaling in taste cells.	
CC	(M1) is useful for identifying a compound that modulates taste signalling	
CC	in taste cells, for identifying a compound that binds to a taste cell	
CC	specific ion channel subunit and for modulating taste signaling in taste	
CC	cells of a mammal, in particular a human. Modulators identified by (M1)	
CC	are used by the food and pharmaceutical industries to customize taste,	
CC	e.g. as additives to food or medicine so that the food or medicine tastes	
CC	different to the subject who ingests it. Bitter medicines can be made to	
CC	taste less bitter and sweet substance can be enhanced. The modulators are	
CC	useful for pharmacological and genetic modulation of taste signalling	
CC	pathways. The taste modulators can be directly administered to mammalian	
CC	subjects for modulation of taste in vivo. The present sequence is that of	
CC	the predicted human ltrpc6 protein of the invention	
XX		
SQ	Sequence 1165 AA;	

Query Match			
Best Local Similarity 100.0%; Score 6093; DB 5; Length 1165;			
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MDVQGP	PRGSGDADREELGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFDLLLAEW 60
Db	1	MDVQGP	PRGSGDADREELGLHGEVNFVGGSGKRGKFRVPSGVAPSVLFDLLLAEW 60
QY	61	HLPA	NLVSVLGGSEOPPFAMKSWLNDVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
Db	61	HLPA	NLVSVLGGSEOPPFAMKSWLNDVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
QY	121	RDHSL	ASTSKVRVAVGASLGRHLHRRILEEAQEDFPVHPEDDGGSGQPLCSLDSNL 180
Db	121	RDHSL	ASTSKVRVAVGASLGRVLRHRLILEEAQEDFPVHPEDDGGSGQPLCSLDSNL 180
QY	181	SHFIL	VEPGPPGKDGTLRLRLSKHISEQRAQYGGTGSIEIPVLCVLLVNGDPNLTLE 240
Db	181	SHFIL	VEPGPPGKDGTLRLRLSKHISEQRAQYGGTGSIEIPVLCVLLVNGDPNLTLE 240
QY	241	SRVQA	APWLLVSGGGIADVLAALVNQPHLLVPKVAEKOPKEKFPKSHFSEWEDIVRW 300
Db	241	SRVQA	APWLLVSGGGIADVLAALVNQPHLLVPKVAEKOPKEKFPKSHFSEWEDIVRW 300
QY	301	KLLQN	ITSHQHLTVYDFEQEGSEELDTVILKALVKACKSHSQSPQDYLDLKLAVAWDR 360
Db	301	KLLQN	ITSHQHLTVYDFEQEGSEELDTVILKALVKACKSHSQSPQDYLDLKLAVAWDR 360
QY	361	VDIA	SEIFNGDVEWKSCDLEVMVDALVSNKPEFVRLFVNGADVADFLYGRLOELYR 420
Db	361	VDIA	SEIFNGDVEWKSCDLEVMVDALVSNKPEFVRLFVNGADVADFLYGRLOELYR 420
QY	421	SVSR	KSLFLDILLQKQEBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLAKDFLQDACRG 480
Db	421	SVSR	KSLFLDILLQKQEBEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLAKDFLQDACRG 480
QY	481	FYQGR	PGDRAAEKPAKPTGQKMLDLNOKSENPMWRDLFLMAVLQNRHEMATYFWAM 540
Db	481	FYQGR	PGDRAAEKPAKPTGQKMLDLNOKSENPMWRDLFLMAVLQNRHEMATYFWAM 540
QY	541	GOE	VAAALACKILKENSHELETAARATREAKYERLALDLFSECVSNSEARAFALLV 600
Db	541	GOE	VAAALACKILKENSHELETAARATREAKYERLALDLFSECVSNSEARAFALLV 600
QY	601	RRNC	WSKTTCLHLATEADAKAFPAHQVQAFLTRIMWGDMAAGTPILRLILGAFCLPALV 660
Db	601	RRNC	WSKTTCLHLATEADAKAFPAHQVQAFLTRIMWGDMAAGTPILRLILGAFCLPALV 660
QY	661	YTNL	ITFSEAPLRTGLDQLDLSLDTKESPLYGLQSRVBEELVEAPRAQGDGRPAVFL 720
Db	661	YTNL	ITFSEAPLRTGLDQLDLSLDTKESPLYGLQSRVBEELVEAPRAQGDGRPAVFL 720
QY	721	LTRM	KFWGAPVTVFLGNVNVYAFLEFTTVLLVDFRPPQSGSEVTVLYFWVFTLV 780
Db	721	LTRM	KFWGAPVTVFLGNVNVYAFLEFTTVLLVDFRPPQSGSEVTVLYFWVFTLV 780
QY	781	BEIR	QGFTEBDTHLVKKFTLYVGDNNKCDMAIFLFIIVGVTCTMLPSAFEAGRTVLAM 840
Db	781	BEIR	QGFTEBDTHLVKKFTLYVGDNNKCDMAIFLFIIVGVTCTMLPSAFEAGRTVLAM 840
QY	841	DFMV	FTLRLIHI FAIHKQLGPKIIVVERMKDVFFLFFLSVWLVAVGVTTQALLPHDG 900
Db	841	DFMV	FTLRLIHI FAIHKQLGPKIIVVERMKDVFFLFFLSVWLVAVGVTTQALLPHDG 900
QY	901	RLEW	IFRVLRYPLQIFGQIPDLDEIDARVNCSTHPLLEDSPCSLSLVANMLVILLV 960
Db	901	RLEW	IFRVLRYPLQIFGQIPDLDEIDARVNCSTHPLLEDSPCSLSLVANMLVILLV 960
QY	961	TFLV	TVNLLMNLIAFSTYFQVQGNADMFKFYRNLIVEYHERPALAPPFILLSHL 1020
Db	961	TFLV	TVNLLMNLIAFSTYFQVQGNADMFKFYRNLIVEYHERPALAPPFILLSHL 1020
QY	1021	SLTL	RRVFKAEHREHLERDLPDLDQKVVTWETVQKENFLSKMEKRRRDSGEVLRK 1080

Db	1021	SLTLRRVFKAEHREKHLERDLPDLQKVVTWETVQKENFLSKMEKRRRDSGEVLRK	1080
QY	1081	TAHRVDFIAKYLGRLREQEKRICKLESQINVCVSVADVLAQGGGPRSSQHCBSG	1140
Db	1081	TAHRVDFIAKYLGRLREQEKRICKLESQINVCVSVADVLAQGGGPRSSQHCBSG	1140
QY	1141	LVAADHRGGLDGWEQPGAGQPPSDT	1165
Db	1141	LVAADHRGGLDGWEQPGAGQPPSDT	1165
RESULT 4			
ID	ADJ69344		
XX	ADJ69344	standard; protein; 1165 AA.	
XX	AC	ADJ69344;	
XX	DT	06-MAY-2004 (first entry)	
XX	XX	Human heat mitochondrial protein as a therapeutic target SeqID1150.	
DE	DE	mitochondrial; human; screening assay; diabetes mellitus;	
XX	XX	Huntington's disease; osteoarthritis;	
KW	KW	Leber's hereditary optic neuropathy; LHON;	
KW	KW	mitochondrial encephalopathy lactic acidosis and stroke; MELAS;	
KW	KW	myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;	
KW	KW	neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;	
KW	KW	osteopathic; ophthalmological; cytostatic.	
XX	OS	Homo sapiens.	
XX	XX	W02003087768-A2.	
PN	XX	23-OCT-2003.	
PD	XX	04-APR-2003; 2003WO-US010870.	
PF	XX	12-APR-2002; 2002US-0372843P.	
PR	XX	17-JUN-2002; 2002US-0389987P.	
PR	XX	20-SEP-2002; 2002US-0412418P.	
XX	XX	(MITO-) MITOKOR.	
PA	PA	(BUCK-) BUCK INST AGE RES.	
XX	PI	Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;	
PI	PI	Warnock DE;	
XX	XX	WPI; 2003-845369/78.	
DR	XX	Identifying a mitochondrial target for drug screening assays and for	
XX	XX	treating diseases associated with altered mitochondrial function,	
PT	PT	comprises detecting a modified polypeptide in a sample and correlating	
PT	PT	with the disease.	
XX	XX	Claim 1; SEQ ID NO 1150; 180pp; English.	
PS	XX	This invention relates to novel mitochondrial targets that can be used	
CC	CC	for therapeutic intervention in treating a disease associated with	
CC	CC	altered mitochondrial function. Specifically, it refers to a method for	
CC	CC	identifying proteins of the human heart mitochondrial proteome that are	
CC	CC	useful for drug screening assays, as well as therapeutic targets. The	
CC	CC	present invention describes a method for identifying such proteins that	
CC	CC	can be used in the treatment of various diseases associated with altered	
CC	CC	mitochondrial function including diabetes mellitus, Huntington's disease,	
CC	CC	osteochondritis, Leber's hereditary optic neuropathy (LHON), mitochondrial	
CC	CC	encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy	
CC	CC	ragged red fibre syndrome (MERRF) or cancer. Accordingly, these	
CC	CC	compositions have neuroprotective, nontropic, antidiabetic,	
CC	CC	anticonvulsant, antiarthritic, osteopathic, ophthalmological and	
CC	CC	cytostatic activities. This polypeptide sequence is a human heart	
CC	CC	mitochondrial protein of the invention.	
XX	XX		

SQ	Sequence 1165 AA;	
Query Match	100.0%; Score 6093; DB 7; Length 1165;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1165; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MDVQGPSPGDAEDRRELGLHGEVNFVGGGKRGKRVVPVSGVAPSVLFDLLAEM 60	
Db	1 MDVQGPSPGDAEDRRELGLHGEVNFVGGGKRGKRVVPVSGVAPSVLFDLLAEM 60	
QY	61 HLPAPNLVSVLGESEQPFAMKSWLRLVLRGLVKAQSTGAWILTSALRGLRHVGQAV 120	
Db	61 HLPAPNLVSVLGESEQPFAMKSWLRLVLRGLVKAQSTGAWILTSALRGLRHVGQAV 120	
QY	121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIEEAQEDFPVHPYEDDGGSGQPLCSLDSNL 180	
Db	121 RDHSLASTSTKRVVAVGMSLGRVLRHRIIEEAQEDFPVHPYEDDGGSGQPLCSLDSNL 180	
QY	181 SHFILLVEPGPGKGLTELRLRLEKHISEORAGYGGTGSIEIPVLCLLVNGDPNLTLE 240	
Db	181 SHFILLVEPGPGKGLTELRLRLEKHISEORAGYGGTGSIEIPVLCLLVNGDPNLTLE 240	
QY	241 SRAVEQAAFWLILVSGGGIADYLAALVNQPHLLVPKVAEKQPKFKPSHFSWEDIVRWT 300	
Db	241 SRAVEQAAFWLILVSGGGIADYLAALVNQPHLLVPKVAEKQPKFKPSHFSWEDIVRWT 300	
QY	301 KLLQNTSHQHLITVDFEQEGSELDVTILKALVKACKSHSQEPQDYLDLKLAVADR 360	
Db	301 KLLQNTSHQHLITVDFEQEGSELDVTILKALVKACKSHSQEPQDYLDLKLAVADR 360	
QY	361 VDIASEIFNGDVEWKSDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR 420	
Db	361 VDIASEIFNGDVEWKSDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR 420	
QY	421 SVSRKSLFLDLQKQEEARLTLAGLGTQQAEPAPGPAFSLHEVSRVLDKFLQDACRG 480	
Db	421 SVSRKSLFLDLQKQEEARLTLAGLGTQQAEPAPGPAFSLHEVSRVLDKFLQDACRG 480	
QY	481 FYQDGRPGDRAEKGPAKPTGQKWLDLNOKSENPRDLFLWAVLQNRHEMATYFWAM 540	
Db	481 FYQDGRPGDRAEKGPAKPTGQKWLDLNOKSENPRDLFLWAVLQNRHEMATYFWAM 540	
QY	541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSARAFALIV 600	
Db	541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSARAFALIV 600	
QY	601 RNRCSKTTCLHLATEADAKAFPAHDGVQAFILTRIWMGDMAGTPIRLLLGAFCLPALV 660	
Db	601 RNRCSKTTCLHLATEADAKAFPAHDGVQAFILTRIWMGDMAGTPIRLLLGAFCLPALV 660	
QY	661 YTNLITFSEAPLRTGLELDQLDLSLDEKSPLYGLQSRVEELVEAPRAQGRGPRAVFL 720	
Db	661 YTNLITFSEAPLRTGLELDQLDLSLDEKSPLYGLQSRVEELVEAPRAQGRGPRAVFL 720	
QY	721 LTRWRKFWGAPTVFLGNVVMYFAFLFTYVLLVDFRPPQPGSPGPEVTLFWVFTLV 780	
Db	721 LTRWRKFWGAPTVFLGNVVMYFAFLFTYVLLVDFRPPQPGSPGPEVTLFWVFTLV 780	
QY	781 EETRQGFDTDEDTHLVKCKFTLVGDMNWKDMVAIFLFTVGVTCRMLPSAFAGRTVLAM 840	
Db	781 EETRQGFDTDEDTHLVKCKFTLVGDMNWKDMVAIFLFTVGVTCRMLPSAFAGRTVLAM 840	
QY	841 DMVFTLRLIHPAIHKQLGPKIIVVERMMKVDFELFLSVMLVAYGVTTQALLPHDGG 900	
Db	841 DMVFTLRLIHPAIHKQLGPKIIVVERMMKVDFELFLSVMLVAYGVTTQALLPHDGG 900	
QY	901 RLEWIFRRVLYRPLQIFQGIPLDEIDARVNCSTHPLLEDSPSPSYANWLVILLV 960	
Db	901 RLEWIFRRVLYRPLQIFQGIPLDEIDARVNCSTHPLLEDSPSPSYANWLVILLV 960	
QY	961 TELLVNTVLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVYHERPALAPPFILLSHL 1020	
Db	961 TELLVNTVLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVYHERPALAPPFILLSHL 1020	

QY	1021 SLTLRRVFKKEAEHREHLERDLPPDLQKQVVTWETVQKFNFLSKMEKRRDRDSEGEVLRK 1080	
Db	1021 SLTLRRVFKKEAEHREHLERDLPPDLQKQVVTWETVQKFNFLSKMEKRRDRDSEGEVLRK 1080	
QY	1081 TAHRVDPIAKYLGRLREQEKRIKLESQINVCYVLSVSVADVLAQGGGPRSSOHCGGSGQ 1140	
Db	1081 TAHRVDPIAKYLGRLREQEKRIKLESQINVCYVLSVSVADVLAQGGGPRSSOHCGGSGQ 1140	
QY	1141 LVAADHRGGLDQWEGOPGAGOPPSSDT 1165	
Db	1141 LVAADHRGGLDQWEGOPGAGOPPSSDT 1165	
RESULT 5		
ADR48686		
ID	ADR48686 standard; protein; 1165 AA.	
XX		
AC	ADR48686;	
XX		
DT	02-DEC-2004 (first entry)	
XX		
DE	Transient receptor potential melastinin-like channel TRPM5 SEQ ID 2.	
XX		
KW	Immunosuppressive; Cytostatic;	
KW	Transient receptor potential melastinin-like channel; TRPM5;	
KW	Calcium-Activated Nonspecific Transmembrane Channel;	
KW	CAN transmembrane channel; ion channel; chromosome 11p15.5;	
KW	autoimmune disorder; graft versus host disease; cancer; human.	
XX		
OS	Homo sapiens.	
XX		
XX		
FT	Misc-difference 2 /note= "Encoded by CNN"	
FT	Misc-difference 14 /note= "Encoded by NNT"	
XX		
PN	WO2004076632-A2.	
XX		
PD	10-SEP-2004.	
XX		
PF	23-FEB-2004; 2004WO-US005316.	
XX		
PR	21-FEB-2003; 2003US-0448955P.	
XX		
PA	(QUBB-) QUEENS MEDICAL CENT.	
XX		
PI	Penner R, Fleig A;	
XX		
DR	WPI: 2004-662007/64.	
DR	N-PSDB; ADR48685.	
XX		
PT	Screening for agent capable of binding to or modulating expression of	
PT	transient receptor potential melastinin-like (TRPM5) polypeptide or	
PT	modulating ionic permeability of TRPM5 channel, useful for treating	
PT	cancer, autoimmune disease.	
XX		
PS	Claim 3; Fig 7; 69pp; English.	
XX		
CC	The present invention relates to a method (M1) for screening for	
CC	candidate bioactive agents (A1) which are capable of: binding to	
CC	transient receptor potential melastinin-like (TRPM5) polypeptide	
CC	(ADR48686); modulating monovalent cationic permeability of channel	
CC	comprising TRPM5 polypeptide; and modulating expression of TRPM5 nucleic	
CC	acid. The method involves contacting TRPM5 polypeptide, channel or cell	
CC	expressing TRPM5 nucleic acid with (A1) and detecting whether (A1) causes	
CC	the required effect. TRPM5 is a member of the differentiating Calcium-	
CC	activated Nonspecific (CAN) transmembrane channel polypeptide family and	
CC	is activated by a rapid increase in intracellular calcium ion (Ca2+)	
CC	levels. The TRPM5 coding sequence (ADR48685) was derived from human	
CC	kidney cells, however, TRPM5 is broadly expressed in various mammalian	
CC	tissues. The presence of TRPM5 in a variety of tissues indicates a	

CC generalised role of the channel as a tool that couples agonist-induced
 CC intracellular Ca2+ release to electrical activity and subsequent cellular
 CC responses. The TRPM5 gene was found to be located on chromosome 11p15.5.
 CC The candidate bioactive agents identified by (M1), which can open TRPM5
 CC channels in a variety of cell such as cells of nervous, immune, and
 CC muscular systems of vertebrates, are useful for treating diseases, and
 CC conditions associated with diseases, or disorders, such as autoimmune or
 CC graft versus host diseases, or other related autoimmune disorders. The
 CC candidate bioactive agents identified by (M1), which can close TRPM5
 CC channels are useful for treating diseases, conditions associated with
 CC diseases, or disorders, such as breast and colon cancer or other forms of
 CC cancer.
 CC
 XX

SQ Sequence 1165 AA;

Query Match	100.0%;	Score 6093;	DB 8;	Length 1165;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1165;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MQDVQPRPGSGDADREDELGLHGEVNFSGGKRGKRVPGVAPSVLFDLLAEW 60
 DB 1 MQDVQPRPGSGDADREDELGLHGEVNFSGGKRGKRVPGVAPSVLFDLLAEW 60
 QY 61 HLPAPNLVSVLGEQPPFAMKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
 DB 61 HLPAPNLVSVLGEQPPFAMKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
 QY 121 RHSLASTSTKRVVAVGASGRVLRHRLIEAQAEDFPVHPEDDGGQGPLCSLDNL 180
 DB 121 RHSLASTSTKRVVAVGASGRVLRHRLIEAQAEDFPVHPEDDGGQGPLCSLDNL 180
 QY 181 SHFILVEPPGPGKGLTELRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDNPNTLRI 240
 DB 181 SHFILVEPPGPGKGLTELRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDNPNTLRI 240
 QY 241 SRAVQAAPWLLVSGGDIADVLAAVLPKVAEKQPKFKPSKHSWEDIVRWT 300
 DB 241 SRAVQAAPWLLVSGGDIADVLAAVLPKVAEKQPKFKPSKHSWEDIVRWT 300
 QY 301 KLLQNTISQHLTLVYDPEQSGSELDVTILKALVKACKSHQSPQDYLDLKLAVADR 360
 DB 301 KLLQNTISQHLTLVYDPEQSGSELDVTILKALVKACKSHQSPQDYLDLKLAVADR 360
 QY 361 VDIASEIFNGDVIEWSKCDLSEVMVDALVSNKPFVRLVDNGADVADFLTYGRLELYR 420
 DB 361 VDIASEIFNGDVIEWSKCDLSEVMVDALVSNKPFVRLVDNGADVADFLTYGRLELYR 420
 QY 421 SVSRKSLFDLLQKQBEARLTLAGLGTQQAAREPPAGPAPSLHEVSRVLKDFLODACRG 480
 DB 421 SVSRKSLFDLLQKQBEARLTLAGLGTQQAAREPPAGPAPSLHEVSRVLKDFLODACRG 480
 QY 481 FYQGRPGDRRAEKGPAKRPFGKWLDDLNQKSENPRDLFLWAVLQNRHEMATYFWAM 540
 DB 481 FYQGRPGDRRAEKGPAKRPFGKWLDDLNQKSENPRDLFLWAVLQNRHEMATYFWAM 540
 QY 541 QGEGVAALAAACKILKEMSHLETAABARATREAKYERLALDLFSECYSNSEARAFALLV 600
 DB 541 QGEGVAALAAACKILKEMSHLETAABARATREAKYERLALDLFSECYSNSEARAFALLV 600
 QY 601 RNRCSWKTTCCLHLATADAKAFPAHDGVQAFRLRIWGDMAAGTPTILRLIGALPCALV 660
 DB 601 RNRCSWKTTCCLHLATADAKAFPAHDGVQAFRLRIWGDMAAGTPTILRLIGALPCALV 660
 QY 661 YTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQDGRPRAVFL 720
 DB 661 YTNLITFSEAPLRTGLDQLDLSLDEKSPLYGLQSRVEELVEAPRAQDGRPRAVFL 720
 QY 721 LTRWRKFWGAPVTVFLGNVVFALFTYVLLVDRPPQPSGSEVTLTYFWFTVLV 780
 DB 721 LTRWRKFWGAPVTVFLGNVVFALFTYVLLVDRPPQPSGSEVTLTYFWFTVLV 780
 QY 781 BEIRQGFTEDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTVLAM 840
 DB 781 BEIRQGFTEDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTVLAM 840

Db	781	BEIRQGFTEDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTVLAM	840
QY	841	DFMVFTELRHIFAIHKQLGPKIIVVERMKDVFFLFFLSVWLVAYGVTTQALLHPHDG	900
Db	841	DFMVFTELRHIFAIHKQLGPKIIVVERMKDVFFLFFLSVWLVAYGVTTQALLHPHDG	900
QY	901	RLEWIFRRVLYRPLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLVANWLVILLV	960
Db	901	RLEWIFRRVLYRPLQIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLVANWLVILLV	960
QY	961	TFLLVTVNVLNMLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPPFILLSHL	1020
Db	961	TFLLVTVNVLNMLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPPFILLSHL	1020
QY	1021	SLTLRRRVFKAEHREHLERDLDPDLQDKVVTWETVQENFLSKMEKRRDSEGEVLRK	1080
Db	1021	SLTLRRRVFKAEHREHLERDLDPDLQDKVVTWETVQENFLSKMEKRRDSEGEVLRK	1080
QY	1081	TAHRVDITAKYLGGLRQEKRIKCLESIQINVCVSVSVADVLAQGGGPRSSQHCGEQS	1140
Db	1081	TAHRVDITAKYLGGLRQEKRIKCLESIQINVCVSVSVADVLAQGGGPRSSQHCGEQS	1140
QY	1141	LVAADHRGGLDGWEOPGAGOPPSDT	1165
Db	1141	LVAADHRGGLDGWEOPGAGOPPSDT	1165

RESULT 6
 ADDR87161
 ID ADDR87161 standard; protein; 1167 AA.
 XX ADDR87161;
 AC ADDR87161;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human betaTRP amino acid sequence, seq id 2.
 XX
 KW Antidiabetic; betaTRP modulator; gene therapy; glucose; insulin; betaTRP;
 KW beta transducin; diabetes; type 2; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 734..757 /note= "Transmembrane region"
 FT Region 771..790 /note= "Transmembrane region"
 FT Region 809..826 /note= "Transmembrane region"
 FT Region 838..857 /note= "Transmembrane region"
 FT Region 875..897 /note= "Transmembrane region"
 FT Region 957..979 /note= "Transmembrane region"
 FT Region 994..999 /note= "Transmembrane region"
 FT Region /note= "TRP motif"
 XX
 PN WO2004079372-A1.
 XX
 PD 16-SEP-2004.
 XX
 PF 04-MAR-2004; 2004WO-US006697.
 XX
 PR 05-MAR-2003; 2003US-0452596P.
 XX
 PA (META-) METABOLEX INC.
 XX
 PI Johnson JD, Zhou Y;
 XX WPI; 2004-668668/65.
 DR N-PSDB; ADDR87160.
 XX

Identifying agents that induce glucose-stimulated insulin production in an animal, useful for treating diabetes, comprises contacting an agent to a polypeptide and selecting an agent that binds or enhances its expression/activity.

Claim 1; SEQ ID NO 2; 83pp; English.

The invention relates to a method for identifying an agent that induces glucose-stimulated insulin production in an animal. The method comprises contacting an agent to a betatRP polypeptide, and selecting an agent that binds to it or enhances its expression or activity. Further disclosed is a method for expressing betatRP (beta-transducin protein) in a pancreatic islet cell. The method is useful for identifying an agent that induces glucose-stimulated insulin production in an animal, and thus treating individuals having type 2 diabetes mellitus or having a predisposition for it. The current sequence represents the human betatRP amino acid sequence.

Sequence 1167 AA;

Query Match	99.8%;	Score 6078;	DB 8;	Length 1167;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1164:	Conservative	1;	Mismatches	0;
	Indels	2;	Gaps	1;

Qy	1	MODVQGRPGSGDAEORRELGJLHRGEVNFVGGSGKKRGKFRVRVPSGVNAPSVLDFLLLAEW	60
Db	1	MODVQGRPGSGDAEORRELGJLHRGEVNFVGGSGKKRGKFRVRVPSGVNAPSVLDFLLLAEW	60
Qy	61	HLPAPNLVSLVGBEQPFAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVGOAV	120
Db	61	HLPAPNLVSLVGBEQPFAMKSWLDRVLKGLVKAQAQSTGAWILTSALRVGLARHVGOAV	120
Qy	121	RDHSLASTSTKVRVVAVGMAISLGRVLHRRILLEEAO--EDFPVHVPEDDGGSGOPLCSLDS	178
Db	121	RDHSLASTSTKVRVVAVGMAISLGRVLHRRILLEEAOVHEDFPVHVPEDDGGSGOPLCSLDS	180
Qy	179	NLSHFILVPEPPGKGDGLTELRLRLKXHISEORAGYGGTGSIEIPVLCLLVNGDPNTLE	238
Db	181	NLSHFILVPEPPGKGDGLTELRLRLKXHISEORAGYGGTGSIEIPVLCLLVNGDPNTLE	240
Qy	239	RISRAVEOAAWLLILVGGSGIADVLAAVLNPHLLVPKVAEKOFKEKPPSKHFSWEDIVR	298
Db	241	RISRAVEOAAWLLILVGGSGIADVLAAVLNPHLLVPKVAEKOFKEKPPSKHFSWEDIVR	300
Qy	299	WTKLLQNTISHQHLLTVYDFEOEGSEELDTVLKALVKACKSHSQEPQDYLDLKLAVAM	358
Db	301	WTKLLQNTISHQHLLTVYDFEOEGSEELDTVLKALVKACKSHSQEPQDYLDLKLAVAM	360
Qy	359	DRVDIAKSEIFNGDVEMKSCDLEEVNVDALVSNKPEFVRLFVDNGADVADFLTLYGRLOEL	418
Db	361	DRVDIAKSEIFNGDVEMKSCDLEEVNVDALVSNKPEFVRLFVDNGADVADFLTLYGRLOEL	420
Qy	419	YRSVSRKSLIPDLLQKQOEAEARLTLAGLGTQOAREPPAGPPAFSLHEVSRVLKDFLODAC	478
Db	421	YRSVSRKSLIPDLLQKQOEAEARLTLAGLGTQOAREPPAGPPAFSLHEVSRVLKDFLODAC	480
Qy	479	RGFYODGPRGDRRAEKGPAKPTGOKWLLDLNOKSENPRDLFLWAVLQNRHEMATYFW	538
Db	481	RGFYODGPRGDRRAEKGPAKPTGOKWLLDLNOKSENPRDLFLWAVLQNRHEMATYFW	540
Qy	539	AMQEGVAAALAAACKILKEMSHLETAEAARATREAKYERLALDLPSECYSNSSEARAPAL	598
Db	541	AMQEGVAAALAAACKILKEMSHLETAEAARATREAKYEQALDLDFSECYSNSSEARAPAL	600
Qy	599	LVRNRNCSKTTCLHLATADAKAPFAHDGVQAFTRIWWGDMMAAGTPTILRLIGAFLCPA	658
Db	601	LVRNRNCSKTTCLHLATADAKAPFAHDGVQAFTRIWWGDMMAAGTPTILRLIGAFLCPA	660
Qy	659	LVYTNLITPSEBAPLTGLEDQLDLSLDTKSPLYGLOSREVELVEAPRAQODRGPRAV	718
Db	661	LVYTNLITPSEBAPLTGLEDQLDLSLDTKSPLYGLOSREVELVEAPRAQODRGPRAV	720
Qy	719	FLLTRWRKFWGAPVTIVFLGNVVMYFAFLFTYTVLLIVDFRPPQPGSGPEVTLYFWVFTL	778

CC (transient receptor potential) family protein; (ii) is connected with
 CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
 CC with tumors involving 11p15.5 abnormalities. The products of the
 CC invention have anticancer and developmental activity. MTR1 is involved in
 CC regulation of intracellular calcium ion levels, which are essential for
 CC cellular responses to hormones and/or growth factors; also in apoptosis
 CC and cell growth, death and differentiation, and in urogenital diseases,
 CC including polycystic kidney disease. (I) and related ribozymes, antisense
 CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
 CC associated with altered expression of the MTR1 gene or activity of its
 CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
 CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
 CC used for diagnosis of such diseases. (I) can also be used for recombinant
 CC production of MTR1 proteins (II) (used for analysis, characterization and
 CC therapy), as tissue or chromosomal markers, for identifying genetic
 CC diseases and related sequences, as primers for genetic fingerprinting, as
 CC source of oligonucleotides for biochips, and to raise anti-protein or
 CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
 CC competitive assays for (II), as tissue markers; for identifying
 CC interacting proteins and in screening for (ant)agonists. This sequence
 CC represents a human MTR1 protein described in the method of the invention
 CC
 XX Sequence 1179 AA;

Query Match 99.0%; Score 6034; DB 4; Length 1179;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1162; Conservative 0; Mismatches 2; Indels 16; Gaps 3;

QY 1 MQDVQCPGSGDADRELGLHRCGEVNFSGGKRGKFRVPSGVAPSVLFDLLAEW 60
 DB 1 MQDVQCPGSGDADRELGLHRCGEVNFSGGKRGKFRVPSGVAPSVLFDLLAEW 60

QY 61 HLPAPNLVSLVGEQEPFAMKWLRLDLKGLVKAQAQSTGAWILTSALRVGLRHVGQAV 120
 DB 61 HLPAPNLVSLVGEQEPFAMKWLRLDLKGLVKAQAQSTGAWILTSALRVGLRHVGQAV 120

QY 121 RHSLASTSTKRVVAVGASLGRVLRHRIIEAEQEDFPVHPEDDGGSGPLCSLSNL 180
 DB 121 RHSLASTSTKRVVAVGASLGRVLRHRIIEAEQEDFPVHPEDDGGSGPLCSLSNL 180

QY 181 SHFILLVEPGPGKDGTLRLRLKHLSEQRAGYGGTSGTIEIPVLCVNGDNTLRI 240
 DB 181 SHFILLVEPGPGKDGTLRLRLKHLSEQRAGYGGTSGTIEIPVLCVNGDNTLRI 240

QY 241 SRAVEQAPWLLVSGGDIADVLAAVNPQHLVVKVAEKQFKKFPKSHFSDIVRWT 300
 DB 241 SRAVEQAPWLLVSGGDIADVLAAVNPQHLVVKVAEKQFKKFPKSHFSDIVRWT 300

QY 301 KLLQNTITSHQHLTVYDFEQSGSELDVILKALVKACKSHSQSPQDYDLDELKLVAVDR 360
 DB 301 KLLQNTITSHQHLTVYDFEQSGSELDVILKALVKACKSHSQSPQDYDLDELKLVAVDR 360

QY 361 VDIKSEIFNGDVEWKSQDLBEVMDALVSNKPFVRLFDVNGADVADFTYGRLOLYR 420
 DB 361 VDIKSEIFNGDVEWKSQDLBEVMDALVSNKPFVRLFDVNGADVADFTYGRLOLYR 420

QY 421 SVSRKSLLDLLOKQEARLTLAGLCTQQAAREPPAGPPAPSLHEVSRVLKQFLQACRG 480
 DB 421 SVSRKSLLDLLOKQEARLTLAGLCTQQAAREPPAGPPAPSLHEVSRVLKQFLQACRG 480

QY 481 FYQDGRPGDRRAEKGPAKRTGQKWLDDLNQKSENPNRDLFLWAVLQNRHENAITYFWAM 540
 DB 481 FYQDGRPGDRRAEKGPAKRTGQKWLDDLNQKSENPNRDLFLWAVLQNRHENAITYFWAM 540

QY 541 QOEGVAALAAACKLLKWSHLETAABAARATREAKYERLAL-----DLFSECYSNSEARA 595
 DB 541 QOEGVAALAAACKLLKWSHLETAABAARATREAKYERLAL-----DLFSECYSNSEARA 595

QY 596 FALLVRRNRCSKTTCLHLATEADAKFAFFADGQVAFTRIWMGDMAGTPIILRLGAGL 655
 DB 601 FALLVRRNRCSKTTCLHLATE -DAKFAFFADGQVAFTRIWMGDMAGTPIILRLGAGL 659

QY 656 CPALVYTNLTTFSEAPLRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQDGRGP 715

DB 660 CPALVYTNLTTFSEAPLRTGLEDLQDLSLDTKSPLYGLQSRVEELVEAPRAQDGRGP 719
 QY 716 RAVFLLTTRKFWGAPVTVFIGNVMVPAFLFTFLTYLLVDPRPPQPGSPGVTLVFWV 775
 DB 720 RAVFLLTTRKFWGAPVTVFIGNVMVPAFLFTFLTYLLVDPRPPQPGSPGVTLVFWV 779
 QY 776 FTLVLEERQCGFFTDDETHLVKKTLLVYGNMKNKDMVAIFLFTVGTCTRMPLPSAFAGR 835
 DB 780 FTLVLEERQCGFFTDDETHLVKKTLLVYGNMKNKDMVAIFLFTVGTCTRMPLPSAFAGR 839
 QY 836 TVLWDMFVFTLRILHIFALHKLGPKEIIVVERMKMDVFFFLFSLVNLVAYGTTQALL 895
 DB 840 TVLWDMFVFTLRILHIFALHKLGPKEIIVVERMKMDVFFFLFSLVNLVAYGTTQALL 899
 QY 896 HPHDGRLEWFRVLYRPIYQIQIQLDEIDARVNCSTHPLLEDSPSCPSLYANWL 955
 DB 900 HPHDGRLEWFRVLYRPIYQIQIQLDEIDARVNCSTHPLLEDSPSCPSLYANWL 959
 QY 956 ILLLVTFLLTVNLLNLLIAMFSYTFQVVGQADMPKFORYNLIVEYHERPALAPFFI 1015
 DB 960 ILLLVTFLLTVNLLNLLIAMFSYTFQVVGQADMPKFORYNLIVEYHERPALAPFFI 1019
 QY 1016 LLSHLSLTLRVPKKEA-----EHKREHLERDLPDLPDQKVVTWETVQENFLSK 1065
 DB 1020 LLSHLSLTLRVPKKEA-----EHKREHLERDLPDLPDQKVVTWETVQENFLSK 1079
 QY 1066 MEKRRRDSGEVLKRTAHRVDFIAKYLGLLREOEKRIKLESQINYSVLVSSVADVLAQ 1125
 DB 1080 MEKRRRDSGEVLKRTAHRVDFIAKYLGLLREOEKRIKLESQINYSVLVSSVADVLAQ 1139
 QY 1126 GGGPRSSQHCQSGSOLVAADHRGGLDGEWQPGAGQPPSDT 1165
 DB 1140 GGGPRSSQHCQSGSOLVAADHRGGLDGEWQPGAGQPPSDT 1179

RESULT 8
 AAB86164
 ID AAB86164 standard; protein; 1158 AA.
 XX AAB86164;
 AC AAB86164;
 XX AAB86164;
 DT 09-AUG-2001 (first entry)
 XX Mouse MTR1 protein.
 DE Mouse MTR1 protein.
 XX MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
 KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
 KW 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
 KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;
 KW cell growth; cell death; cell differentiation; urogenital disease;
 KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
 KW rhabdomyosarcoma.
 XX Mus sp.
 OS Mus sp.
 XX WO200132693-A2.
 PN WO200132693-A2.
 XX 10-MAY-2001.
 PD 10-MAY-2001.
 XX 06-NOV-2000; 2000WO-DE003876.
 PF 06-NOV-2000; 2000WO-DE003876.
 XX 04-NOV-1999; 99DE-01053167.
 PR 04-NOV-1999; 99DE-01053167.
 XX (UYGU-) UNIV GUTENBERG JOHANNES.
 PA Prawditt D, Pelletier J, Zabel B;
 PI WPI; 2001-316417/33.
 XX WPI; 2001-316417/33.
 DR N-PSDB; AAH20623.
 XX DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
 PT syndrome and tumors, also related proteins and antibodies.

XX PS Disclosure; SEQ ID NO 4; 83pp; English.

XX CC The invention relates to a method for identifying an agent that induces

XX CC glucose-stimulated insulin production in an animal. The method comprises

XX CC contacting an agent to a betaTRP polypeptide, and selecting an agent that

XX CC binds to it or enhances its expression or activity. Further disclosed is

XX CC a method for expressing betaTRP (beta-transducin protein) in a pancreatic

XX CC islet cell. The method is useful for identifying an agent that induces

XX CC glucose-stimulated insulin production in an animal, and thus treating

XX CC individuals having type 2 diabetes mellitus or having a predisposition

XX CC for it. The current sequence represents the mouse betaTRP amino acid

XX CC sequence.

XX SQ Sequence 1158 AA;

Query Match 83.5%; Score 5088.5; DB 8; Length 1158;

Best Local Similarity 84.1%; Pred. No. 0;

Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MDVQGPGRSGDADREELCHLRGEVNFSGGKRGKFKVVRPSGAPSVLFDLLAEW 60

DB 1 MQTQSSCFSPDDEGWEPILCRGEINFGSGKRGKFKVVRPSGAPSVLFEILLTEW 60

QY 61 HLPAPNLVSVLGEERPLANKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGQAV 120

DB 61 HLPAPNLVSVLGEERPLANKSWLRDLVLRKGLVKAQSTGAWILTSALRVGLARHVGQAV 120

QY 121 RDHSLASTSTKVRVAVGNASLGRVLRHRLRILE--EAQEDFPVHYVEDDGGSGPLCSLDS 178

DB 121 RDHSLASTSTKVRVAVGNASLGRVLRHRLRILE--EAQEDFPVHYVEDDGGSGPLCSLDS 178

QY 179 NLSHFILVEPPGKG-DGLTELRLRLKXHSQAGYCGTGSIEIPVLCILVNGDNTL 237

DB 181 NLSHFILVEPPGKG-DGLTELRLRLKXHSQAGYCGTGSIEIPVLCILVNGDNTL 237

QY 238 ERISRAVEQAAPWLLIIVGGGADVLAALVNPHLLVPKVAEKQKPKSPKXHFWEIV 297

DB 241 ERISRAVEQAAPWLLIIVGGGADVLAALVNPHLLVPKVAEKQKPKSPKXHFWEIV 297

QY 298 RWTKLQNTSHQHLITVDYDFEQEGSEELDTVLKALVRACKSHSQEPQDYLDLKLAVA 357

DB 301 HWTCLQNTSHQHLITVDYDFEQEGSEELDTVLKALVRACKSHSQEPQDYLDLKLAVA 357

QY 358 WRVDIAKSEIFNGDVEWKSCLLEEVNVDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 417

DB 361 WRVDIAKSEIFNGDVEWKSCLLEEVNVDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 417

QY 418 LYRSVRSKSLPDLQKQKOEAEARLTAGLTQQAEPAPGAPFSLHEVSRVLKDFLODA 477

DB 421 LYRSVRSKSLPDLQKQKOEAEARLTAGLTQQAEPAPGAPFSLHEVSRVLKDFLODA 477

QY 478 CRGFYQDGRPGDRRAEKGPAKPTQCKWLLDNOKSENPRDLFLWAVLQNRHMYTF 537

DB 481 CRGFYQDGRPGDRRAEKGPAKPTQCKWLLDNOKSENPRDLFLWAVLQNRHMYTF 537

QY 538 WAMQEGVAAALAAKIKEMSHLETAEAEATREAKYERLALDLFSECYNSSEARAF 597

DB 537 WAMQEGVAAALAAKIKEMSHLETAEAEATREAKYERLALDLFSECYNSSEARAF 597

QY 598 LLVRRNRCKSTTCLHLATEADAKAFPAHGDVQAFILTRIWGDMAAGTPTILRLGAPLCP 657

DB 597 LLVRRNRCKSTTCLHLATEADAKAFPAHGDVQAFILTRIWGDMAAGTPTILRLGAPLCP 657

QY 658 ALVYTNLITFSEBAPLRTGLDQLDLSLDEKSPGLYGLQSRVEELVEAPRAGQDRGPA 717

DB 657 ALVYTNLITFSEBAPLRTGLDQLDLSLDEKSPGLYGLQSRVEELVEAPRAGQDRGPA 717

QY 718 VFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTVLLVDRPPPPQSGSEVTLTYFWVFT 777

DB 717 VFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTVLLVDRPPPPQSGSEVTLTYFWVFT 777

QY 778 LVLEERIQGFETDTHLVKFTLYVEDNWNKCDMVAIFLIVGVTCTRMVPSFEAGRTV 837

DB 777 LVLEERIQGFETDTHLVKFTLYVEDNWNKCDMVAIFLIVGVTCTRMVPSFEAGRTV 836

QY 838 LAMDFWFTLRLLIHPAIIKQKQKIIIVVERMKDVEFFLFFLSVWLVAVGVTQTALHP 897

DB 837 LAMDFWFTLRLLIHPAIIKQKQKIIIVVERMKDVEFFLFFLSVWLVAVGVTQTALHP 896

QY 898 HDGRLEWIFRRVLYRYPYQIFGQIPDEIDEARVNCSTHPLLLDESDSCPSLYANWLVL 957

DB 897 HDGRLEWIFRRVLYRYPYQIFGQIPDEIDEARVNCSTHPLLLDESDSCPSLYANWLVL 956

QY 958 LLVTFLLVTVNLLMNLIIAMPSTYFQVQGNADMFKEQRYNVLIVEHERPALAPPFTLL 1017

DB 957 LLVTFLLVTVNLLMNLIIAMPSTYFQVQGNADMFKEQRYNVLIVEHERPALAPPFTLL 1016

QY 1018 SHLSILTRRVKPEAEHRELDLPDLDQKVVTWETVQENFLSKMEKRRDRDSEGEV 1077

DB 1017 SHLSILTRRVKPEAEHRELDLPDLDQKVVTWETVQENFLSKMEKRRDRDSEGEV 1076

QY 1078 LRKTAHRVDFIATKYLGLREQEKIKCLESQINVCVSVLVSVADVLAQGGPRSSQHCGE 1137

DB 1077 LRKTAHRVDFIATKYLGLREQEKIKCLESQINVCVSVLVSVADVLAQGGPRSSQHCGE 1136

QY 1138 GSQVLAADHRCGLDGEQPGAGQPPSDT 1165

DB 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 11

AA886166

ID AA886166 standard; protein; 1158 AA.

XX AC AA886166;

XX DT 09-AUG-2001 (first entry)

XX DE Mouse MTR1 protein #2.

XX KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;

XX KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;

XX KW lip15.5 abnormality; chromosome 11; anticancer; developmental activity;

XX KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;

XX KW cell growth; cell death; cell differentiation; urogenital disease;

XX KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;

XX KW rhabdomyosarcoma.

XX OS Mus sp.

XX PN WO200132693-A2.

XX PD 10-MAY-2001.

XX PF 06-NOV-2000; 2000WO-DE003876.

XX PR 04-NOV-1999; 99DE-01053167.

XX PA (UYGU-) UNIV GUTENBERG JOHANNES.

XX PI Prawitt D, Pelletier J, Zabel B;

XX DR WPI; 2001-316417/33.

XX PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann

XX PT syndrome and tumors, also related proteins and antibodies.

XX PS Disclosure; Fig 12; 46pp; German.

XX CC This invention describes a novel DNA sequence (I) encoding the MTR1

XX CC protein that: (i) has at least one biological activity of a TRP

XX CC (transient receptor potential) family protein; (ii) is connected with

XX CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected

XX CC with tumors involving lip15.5 abnormalities. The products of the

XX CC invention have anticancer and developmental activity. MTR1 is involved in

regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis and cell growth, death and differentiation, and in urogenital diseases, including polycystic kidney disease. (I) and related ribozymes, antisense RNA, proteins and antibodies (Ab)) are used to treat or prevent diseases associated with altered expression of the MTR1 gene or activity of its protein, or with calcium influx into cells, e.g. BWS, Wilms tumor, thalidomide tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also used for diagnosis of such diseases. (I) can also be used for recombinant production of MTR1 proteins (II) (used for analysis, characterization and therapy), as tissue or chromosomal markers, for identifying genetic diseases and related sequences, as primers for genetic fingerprinting, as source of oligonucleotides for biochips, and to raise anti-protein or anti-DNA antibodies. (II) are used to raise Ab, as reagents in competitive assays for (II), as tissue markers; for identifying interacting proteins and in screening for (ant)agonists. This sequence represents the murine MTR1 gene described in the method of the invention

Sequence 1158 AA;

Query Match 83.4%; Score 5080.5; DB 4; Length 1158;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 981; Conservative 67; Mismatches 107; Indels 13; Gaps 4;

QY 1 MQDVQPRGSGDADREELGHRGEVNFSGGKRGKRVVPVSGVAPSVLFDLLAEW 60
DB 1 MQTQSSCGSPDTEGWEPILCRGEINFGSGKRGKRVVPVSGVAPSVLFDLLAEW 60
QY 61 HLPAPNLVSVLGEERPLAMKSWLRLKGLVKAQSTGAWILTSALRVGLRHVGQAV 120
DB 61 HLPAPNLVSVLGEERPLAMKSWLRLKGLVKAQSTGAWILTSALRVGLRHVGQAV 120
QY 121 RHSLASTSKVRVAVGASLGRVLRHRIE--EAQEDFPVHYDEDDGGQGLCSLDS 178
DB 121 RHSLASTSKVRVAVGASLGRVLRHRIE--EAQEDFPVHYDEDDGGQGLCSLDS 178
QY 179 NLSHFTLVEPPGKG-DGLTELRLEKHISEQAGYGGTGSIEIPVLCILLVNDPNTL 237
DB 181 NLSHFTLVEPPGKG-DGLTELRLEKHISEQAGYGGTGSIEIPVLCILLVNDPNTL 240
QY 238 ERISRAVEQAAPWLLVSGGGIADVLAALVNQPHLLVPKAEKOPKEKFPSPKSHSWEDIV 297
DB 241 ERISRAVEQAAPWLLVSGGGIADVLAALVNQPHLLVPKAEKOPKEKFPSPKSHSWEDIV 300
QY 298 RWTLLQNTSHQHLITVDFEQEGSEBELDVTILKALVKACKSHSQEPQDYDLKLAVA 357
DB 301 HWTLLQNTSHQHLITVDFEQEGSEBELDVTILKALVKACKSHSQEPQDYDLKLAVA 360
QY 358 WDRVDIAKSEIFNGDVVEKSCDLEVMYDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 417
DB 361 WDRVDIAKSEIFNGDVVEKSCDLEVMYDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 420
QY 418 LYRSVSRKSLFLDLQKQOEARLTLAGLGTQQAAREPPAGPAPFSLHEVSRVLKDFLODA 477
DB 421 LYHSVSPKSLFLDLQKQOEARLTLAGLGTQQAAREPPAGPAPFSLHEVSRVLKDFLODA 480
QY 478 CRGFYQDGRPGDRRAEAKPRTGQKWLJDLNOKSENPMRDLFLWAVLQNRHEMATYF 537
DB 481 CRGFYQDGRPGDRRAEAKPRTGQKWLJDLNOKSENPMRDLFLWAVLQNRHEMATYF 536
QY 538 WAMQEGVAAALAAACKILKENSHELETAARAAATREAKYERIALDLFSECVSSEARAPA 597
DB 537 WAMQEGVAAALAAACKILKENSHELETAARAAATREAKYERIALDLFSECVSSEARAPA 596
QY 598 LLVRRNCWSITTCILHATEADAKAFPAHDGQVQAFLTRIWMGDMAAGTPIRLIGAFPLCP 657
DB 597 LLVRRNCWSITTCILHATEADAKAFPAHDGQVQAFLTRIWMGDMAAGTPIRLIGAFPLCP 656
QY 658 ALVTNLTTFSEAPLRTGLDLDLSLDEKSPVLYGLSRVEELVEAPRAQDGRPA 717
DB 657 ALVTNLTTFSEAPLRTGLDLDLSLDEKSPVLYGLSRVEELVEAPRAQDGRPA 716
QY 718 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPPQSGSEVTLFWVFT 777

DB 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPPQSGSEVTLFWVFT 776
QY 778 LVLBEIRQGFDTDBDTHLVKFTLYVGDNNKNCMDVAIFLFIYGVTCRMLPSAFAEGRTV 837
DB 777 LVLBEIRQGFDTDBDTHLVKFTLYVGDNNKNCMDVAIFLFIYGVTCRMLPSAFAEGRTV 836
QY 838 LAMDPMVFTLRLIHFAIHKQLGPKIIIVVERMMKDVFFLFFLSVNLVAYGVTTQALLHP 897
DB 837 LAIDPMVFTLRLIHFAIHKQLGPKIIIVVERMMKDVFFLFFLSVNLVAYGVTTQALLHP 896
QY 898 HDGRLWIFRRVLYRVPYLOIFGQIPDEIDEARVNCSTHLLLEDSPSCSLYANMLVIL 957
DB 897 HDGRLWIFRRVLYRVPYLOIFGQIPDEIDEARVNCSTHLLLEDSPSCSLYANMLVIL 956
QY 958 LLVTFLVTVNLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVEVHERPALAPPILL 1017
DB 957 LLVTFLVTVNLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVEVHERPALAPPILL 1016
QY 1018 SHLSLTLRRVPKAEHREHLERDLPDLDQKVVTWETVQENFLSKMEKRDRDSEGEV 1077
DB 1017 SHLSLTLRRVPKAEHREHLERDLPDLDQKVVTWETVQENFLSKMEKRDRDSEGEV 1076
QY 1078 LRKTAHRVDIAKYVGLGRLREQEKRIKCLSEIQINVCVLYSSVADVLAQGGPRSSQHCGE 1137
DB 1077 LRKTAHRVDIAKYVGLGRLREQEKRIKCLSEIQINVCVLYSSVADVLAQGGPRSSQHCGE 1136
QY 1138 GSQIVAADHRGGLDGMWEGQAGQPPSDT 1165
DB 1137 RSQPASARDREYLE-----SGLPPSDT 1158
RESULT 12
AAMS1707
ID AAMS1707 standard; protein; 1157 AA.
XX AAMS1707;
AC AC
DT 16-JAN-2002 (first entry)
DX Mouse TRP8.
DE Mouse; human; TRP8; transient receptor potential channel;
XX taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;
KW pharmaceutical.
XX OS Mus sp.
XX Key Location/Qualifiers
FH Misc-difference 467
FT /note= "Encoded by CACGAG"
XX WQ200179448-A2.
XX 25-OCT-2001.
XX 17-APR-2001; 2001WO-US012608.
XX 17-APR-2000; 2000US-0197491P.
PR 13-APR-2001; 2001US-00834792.
XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX Margolskee RF, Huang L, Rong M, Max M, Perez CA;
XX WPI: 2002-017608/02.
DR N-PSDB; AA199707.
XX A new transient receptor potential channel, designated TRP8, is expressed
PT in taste receptor cells and associated with perception of bitter and
PT sweet taste, and is useful to find new flavor enhancers.
XX Claim 8; Fig 2; 55pp; English.
PS

XX The invention relates to a mouse and human transient receptor potential
CC channel, TRP8, expressed in taste receptor cells and associated with the
CC perception of bitter and sweet taste. Modulators of TRP8 are useful as
CC flavour enhancers in foods, beverages and pharmaceuticals
XX
SQ Sequence 1157 AA;
Query Match 83.3%; Score 5073; DB 5; Length 1157;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 981; Conservative 67; Mismatches 106; Indels 14; Gaps 5;
Qy 1 MODVQPPGPGDAEDRRLGLHGEVNFVGGSGKRGKFKVRVPSGVNAPSVLFDLLAEW 60
Db 1 MOTTQSSCGFPPTDDEWEPILCEGNEFGSGKRGKFKVVPSSVAPSVLFEILLTEW 60
Qy 61 HLPAPNLVSVLGEERPPAMKSWLRLVRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120
Db 61 HLPAPNLVSVLGEERPLAMKSWLRLVRLKGLVKAQSTGAWILTSALRVGLARHVQAV 120
Qy 121 RDHSLASTSTKRVVAVGASLGRVILHRIILE--EAQEDFPVHYPEDDGGSGPLCSLDS 178
Db 121 RDHSLASTSTKRVVAVGASLGRVILHRIILE--EAQEDFPVHYPEDDGGSGPLCSLDS 180
Qy 179 NLSHFILVEPGPPGKG-DGLTELRLRLEKHISEQAGYGGTGISBIPVLCILLVNGDPNTL 237
Db 181 NLSHFILVESGALSGNDGLTELQSLKHISQQRTGTYGTCIQIPVLCILLVNGDPNTL 240
Qy 238 ERISRAVEQAAPWLLVSGGGIADVLAALVNPHLLVPKVAEKQKPKFPSPKHSFWDIV 297
Db 241 ERISRAVEQAAPWLLVSGGGIADVLAALVSPHLLVPQVAEKQPREKFPSECFSEWAI 300
Qy 298 RWTKLLQNTSHOHLTVYDFPQESGELDTVILKALVKAESHQEPQDYLDLKLAVA 357
Db 301 HMTLLQNTIAHPHLLTVYDFPQESGELDTVILKALVKAESHQEAQDYLDLKLAVA 360
Qy 358 WDRVDIAKSEIEFNGDVENKSCDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOE 417
Db 361 WDRVDIAKSEIEFNGDVENKSCDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOE 420
Qy 418 LYRSVSRKSLLDLQKQKOEALTLAGLTQQAAREPPAGPPAFSLHVSRYLKDPLQDA 477
Db 421 LYHSVSPKSLDFELLQKHEEGRLTLAGLGAQAARELPGLPFAFLH-VSRVLDKDFLHDA 479
Qy 478 CRGFYODGPRDRRAEKPAKRPCTGQKWLIDLNKSENPRDPLFVAVLQNRHEMATYF 537
Db 480 CRGFYQDG---RRMEERGPKRPAQKWLPLSRKSEDPWRDLFLVAVLQNRHEMATYF 535
Qy 538 WAMQEGVAAALAAACKILKEMSHLETEAEARATREAKYERLALDLFSECYNSSEARAPA 597
Db 536 WAMQEGVAAALAAACKILKEMSHLETEAEARATREAKYERLALDLFSECYNSSEARAPA 595
Qy 598 LLVRRNRCSKTKLHLATEADAKAFHAGDGVQAFTRIWWGDMAGTPIRLLLGAFCLCP 657
Db 596 LLVRRNHSRITCLHLATEADAKAFHAGDGVQAFTRIWWGDMAGTPIRLLLGAFCTCP 655
Qy 658 ALVYTNLTTFSEAPRLTGLELDLQDLSLDEKSPLYGLQSRVVEELVAPRAGDRGPPRA 717
Db 656 ALIYTNLTTFSEAPRQMDLEDLQEPDLSLDEKSFCLSRGGQLKLEAPRAPAGDLGPPA 715
Qy 718 VELLTTRWRKFWGAPVTFLGNVVMYFAFLFTYVLLVDFRPPQPGSPGSEVTLXFWVFT 777
Db 716 AFLTTRWRKFWGAPVTFLGNVVMYFAFLFTYVLLVDFRPPQPGSPGSEVTLXFWVFT 775
Qy 778 LVLEERIQGFPTDTHLVKFTLYYGDNNKCDMVAIFLIVGVTCRMLPSAFAGRTV 837
Db 776 LVLEERIQGFPTDTHLVKFTLYYEDNWNKCDMVAIFLIVGVTCRWVPSVFEAGRTV 835
Qy 838 LAMDFWVFTLRLIHI FAIHKQLGPKIIVVERMMKDVFFFLFVSVMLVAYGVTTQALLHP 897
Db 836 LAIDFWVFTLRLIHI FAIHKQLGPKIIVVERMMKDVFFFLFVSVMLVAYGVTTQALLHP 895
Qy 898 HDGRLEWIFRRVLYRPLYQIFGQIPDEIDEARVNCSTHPLLEDSPSCPSLVANWLVIL 957

Db 896 HDGRLEWIFRRVLYRPLYQIFGQIPDEIDEARVNCSTHPLLEDSPSCPSLVANWLVIL 955
Qy 958 LLVTELLAVTNVLLMNLIIAMFSYTFVQVQGNADMFKFORYNLIVYHERPALAPPFILL 1017
Db 956 LLVTELLAVTNVLLMNLIIAMFSYTFVQVQGNADMFKFORYNLIVYHERPALAPPFILL 1015
Qy 1018 SHLSLTLRRYFKKEAEHREHLERDLPDLDQKVVTVETVOKENFLSKMKRRRDSGEV 1077
Db 1016 SHLSVLVKQVFRKEAQHRLERDLPDLDQKIITWETVOKENFLSKMKRRRDSGEV 1075
Qy 1078 LRKTAHRVDIAKVLGRLREQEKRIKLESQINVCVSVLSSVADVLQAGGSPRSSOHCGE 1137
Db 1076 LRKTAHRVDIAKVLGRLREQEKRIKLESQINVCVSVLSSVADVLQAGGSPRSSOHCGE 1135
Qy 1138 GSQLVAAADHRGGLDGEQPGAGQPPSDT 1165
Db 1136 RSQPASARDREYLE-----SGLPPSDT 1157
RESULT 13
ADR87165
ID ADR87165 standard; protein; 1156 AA.
XX ADR87165;
XX AC
XX 02-DEC-2004 (first entry)
XX Rat betaTRP amino acid sequence, seq id 6.
DE Antidiabetic; betaTRP modulator; gene therapy; glucose; insulin; betaTRP;
XX Antidiabetic; betaTRP modulator; gene therapy; glucose; insulin; betaTRP;
KW beta transducin; diabetes; type 2; rat.
XX Rattus sp.
OS WO2004079372-A1.
XX 16-SEP-2004.
XX 04-MAR-2004; 2004WO-US006697.
XX 05-MAR-2003; 2003US-0452596P.
XX (META-) METABOLEX INC.
XX Johnson JD, Zhou Y;
XX WPI; 2004-668668/65.
XX N-PSDB; ADR87164.
XX Identifying agents that induce glucose-stimulated insulin production in
an animal, useful for treating diabetes, comprises contacting an agent to
a polypeptide and selecting an agent that binds or enhances its
expression/activity.
XX Disclosure; SEQ ID NO 6; 83pp; English.
XX The invention relates to a method for identifying an agent that induces
glucose-stimulated insulin production in an animal. The method comprises
contacting an agent to a betaTRP polypeptide, and selecting an agent that
binds to it or enhances its expression or activity. Further disclosed is
a method for expressing betaTRP (beta-transducin protein) in a pancreatic
islet cell. The method is useful for identifying an agent that induces
glucose-stimulated insulin production in an animal, and thus treating
individuals having type 2 diabetes mellitus or having a predisposition
for it. The current sequence represents the rat betaTRP amino acid
sequence.
XX Sequence 1156 AA;
Query Match 82.5%; Score 5025.5; DB 8; Length 1156;
Best Local Similarity 83.0%; Pred. No. 0;
Matches 968; Conservative 75; Mismatches 112; Indels 11; Gaps 3;

Db 9 MPMAQSSCFSPPTDGDWEPVLCKGEVNFSGSKRSKFVKVSNVAPSMLELLTTEW 68
Qy 61 HLPAPNLVSVBGEQPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRGLARHVQAV 120
Db 69 HLPAPNLVSVBGEQPFAMKSWLRDLVRKGLVAAQSTGAWILTSALRGLARHVQAV 128
Qy 121 RDHSLASTSTKRVVAVGMAISGRVLRHRIIEEAQEDPPVHPDDGGSGQPLCLSDSNL 180
Db 129 RDHSLASTSTKRVVAVGMAISGRVLRHRIIEEAQEDPPVHPDDGGSGQPLCLSDSNL 188
Qy 181 SHFILVEPPGKG-DGILTELRLRLKELHISORAGYGGTGSIEIPVLCVLLVNGDPNTLER 239
Db 189 SHFILVEPTGSGNDGLAEQLSLEKHSIQRTGYGGTSSIQIPVLCVLLVNGDPSTLER 248
Qy 240 ISRAVEQAAPMLILVSGGIDVLAALVNQPHLLVPKVAEQFKKFPKSPKSHFSDIVRW 299
Db 249 MSRAVEQAAPMLILAGSGGIADVLAALVQPHLLVPQVTEKQFKEPSECFSEWAI VHW 308
Qy 300 TKLLONITSHQHLLTVYDFEQEGSELDVTILKALVAKCKSHSQBPQDYLDLKLAVAMD 359
Db 309 TELQNIAAHPHLLTVYDFEQEGSELDVTILKALVAKCKSHSRDAQDYLDLKLAVAMD 368
Qy 360 RVDIAKSEIFNGDVEKWSCDLEEVNMDALVSNKPEFVRLFDVNGDADVADFLTYGRLOELY 419
Db 369 RVDIAKSEIFNGDVEKWSCDLEEVNMDALVSNKPEFVRLFDVNGDADVADFLTYGRLOELY 428
Qy 420 RSVSRKSLFOLLQKQBEARLTLAGLGTQQAAREPPAGPPAPSLHEVSRVLKDFLODACR 479
Db 429 HVSVPKSLFELLERKHEEGRLLTAGLGAQQRKLPVGLPAPSLHEVSRVLKDFLODACR 488
Qy 480 GRYQGRPGDRRAEKPAKRTGQKWLIDLNKSENPRDLFLWAVLQNRHEMATYFWA 539
Db 489 GRYQGRPGDRRAEKPAKRTGQKWLIDLNKSENPRDLFLWAVLQNRHEMATYFWA 544
Qy 540 MGOEGVAAALACKILKEMSHLETAEARARAREAKYERLALDLFSECVSNSEARAFALL 599
Db 545 MGOEGVAAALACKILKEMSHLETAEARARAREAKYERLALDLFSECVSNSEARAFALL 604
Qy 600 VRRNRCSKTTCLHLATEADAKAFPAHGVQVAPLTRIWMGDMAAGTPIRLILGALCPAL 659
Db 605 VRRNRCSKTTCLHLATEADAKAFPAHGVQVAPLTRIWMGDMAAGTPIRLILGALCPAL 664
Qy 660 VTNLITPSEAPLRTGLDQLDLSLDEKSPGLQSRVELVEAPRAQDGRPAV 719
Db 665 IYTNLITPSEAPLRTGLDQLDLSLDEKSPGLQSRVELVEAPRAQDGRPAV 724
Qy 720 LLTRWRKFGAPVTVPFLGNVVMYFAFLFTVTVLLVDFRPPQPGSGPVTLYFWVFTLV 779
Db 725 LLTRWRKFGAPVTVPFLGNVVMYFAFLFTVTVLLVDFRPPQPGSGPVTLYFWVFTLV 784
Qy 780 LBEIRQGFDTEDTHLVKFTLVYVGNMKNCDMAIFLFIIVGTCRMLPSAFEAGTVLA 839
Db 785 LBEIRQGFDTEDTHLVKFTLVYVGNMKNCDMAIFLFIIVGTCRMLPSAFEAGTVLA 844
Qy 840 MFMVFTLRIHIFAIHKGOLPKPIIIVRRMKDVFLLFSLVWLVAAGVTTQALLPHPD 899
Db 845 IDPMVFTLRIHIFAIHKGOLPKPIIIVRRMKDVFLLFSLVWLVAAGVTTQALLPHPD 904
Qy 900 GRLEWIFRVLRYPLQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVLILL 959
Db 905 GRLEWIFRVLRYPLQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVLILL 964
Qy 960 VTELLVTNLLNLLIAMFSTYFQVQGNADMFKEQRYNLIIVEYHERPALAPPPFILLSH 1019
Db 965 VTELLVTNLLNLLIAMFSTYFQVQGNADMFKEQRYNLIIVEYHERPALAPPPFILLSH 1024
Qy 1020 LSLTLARVFKKEAHEKREHLERDLPDLPDQKVTWETVQENFLSKWEKRRRDSSEVL 1079
Db 1025 LSLVLQVFRKEAHEKREHLERDLPDLPDQKVTWETVQENFLSKWEKRRRDSSEVL 1084
Qy 1080 KTAHRVDPIAKYGLGLEQEKRIKCLSEQINYSVLVSSVADVLAQGGGPRSSQHCES 1139

Db 1085 KTAHRVDPIAKYGLGLEQEKRIKCLSEQINYSVLVSSVADVLAQGGGPRSSQHCES 1144
Qy 1140 QLVAADHRGCLDQWEQPGAGQPPSDT 1165
Db 1145 QPASARDREYLE-----AGLPHSDT 1164
RESULT 15
AAB86163
ID AAB86163 standard; protein; 872 AA.
XX
AC AAB86163;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human MTR1 protein without exon 18 fragment.
XX
KW MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
KW transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;
KW lip15.5 abnormality; chromosome 11; anticancer; developmental activity;
KW intracellular calcium ion regulation; hormone; growth factor; apoptosis;
KW cell growth; cell death; cell differentiation; urogenital disease;
KW polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
KW rhabdomyosarcoma.
XX
OS Homo sapiens.
XX
PN W0200132693-A2.
XX
PD 10-MAY-2001.
XX
PF 06-NOV-2000; 2000WO-DE003876.
XX
PR 04-NOV-1999; 99DE-01053167.
XX
PA (UYGU-) UNIV GUTENBERG JOHANNES.
XX
PI Prawitt D, Pelletier J, Zabel B;
XX
DR WPI; 2001-316417/33.
XX
DR N-PSDB; AAH20574.
XX
PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
XX syndrome and tumors, also related proteins and antibodies.
XX
PS Claim 10; Fig 4; 46pp; German.
XX
CC This invention describes a novel DNA sequence (I) encoding the MTR1
CC protein that: (i) has at least one biological activity of a TRP
CC (transient receptor potential) family protein; (ii) is connected with
CC etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC with tumors involving lip15.5 abnormalities. The products of the
CC invention have anticancer and developmental activity. MTR1 is involved in
CC regulation of intracellular calcium ion levels, which are essential for
CC cellular responses to hormones and/or growth factors; also in apoptosis
CC and cell growth, death and differentiation, and in urogenital diseases,
CC including polycystic kidney disease. (I) and related ribozymes, antisense
CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
CC associated with altered expression of the MTR1 gene or activity of its
CC protein, or with calcium influx into cells, e.g. BWS, Wilms tumor,
CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
CC used for diagnosis of such diseases. (I) can also be used for recombinant
CC production of MTR1 proteins (II) (used for analysis, characterization and
CC therapy), as tissue or chromosomal markers, for identifying genetic
CC diseases and related sequences, as primers for genetic fingerprinting, as
CC source of oligonucleotides for biochips, and to raise anti-protein or
CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
CC competitive assays for (II), as tissue markers; for identifying
CC interacting proteins and in screening for (ant)agonists. This sequence
CC represents a human MTR1 protein described in the method of the invention
XX
SQ Sequence 872 AA;

Query Match		74.4%	Score 4534;	DB 4;	Length 872;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 869;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MQDVQGRPGSGDADRRRLGLHGEVNFVGGGKRGKRVVPVSGVAPSVLFDLLLAEM	60		
Db	1	MQDVQGRPGSGDADRRRLGLHGEVNFVGGGKRGKRVVPVSGVAPSVLFDLLLAEM	60		
Qy	61	HLFAPNLVSLVGEOPFAMKSWLRDLVRKGLVKAAGSTGAMILTSALRVGLARHVQAV	120		
Db	61	HLFAPNLVSLVGEOPFAMKSWLRDLVRKGLVKAAGSTGAMILTSALRVGLARHVQAV	120		
Qy	121	RDHSLASTSTKRVAVAGMASLGRVLRHRLLEAEQEDFPVHYPEDDGGSGGPLCSLDSNL	180		
Db	121	RDHSLASTSTKRVAVAGMASLGRVLRHRLLEAEQEDFPVHYPEDDGGSGGPLCSLDSNL	180		
Qy	181	SHFILVEPPGPGKGDGLTELRLRLEKHISEQRAGYGGTGSIBIPVLCILVNGDPNLTLERI	240		
Db	181	SHFILVEPPGPGKGDGLTELRLRLEKHISEQRAGYGGTGSIBIPVLCILVNGDPNLTLERI	240		
Qy	241	SRAVEQAAPWLIILVSGGGIADVLAAVNOPHLLVPKVAEKQPKPKPSKHSFWSWEDIVRWT	300		
Db	241	SRAVEQAAPWLIILVSGGGIADVLAAVNOPHLLVPKVAEKQPKPKPSKHSFWSWEDIVRWT	300		
Qy	301	KLLQNTTSHQHLTVYDFEQEGSEELDTVILKALVKACKSHSQEQPDYLDLKLAVADR	360		
Db	301	KLLQNTTSHQHLTVYDFEQEGSEELDTVILKALVKACKSHSQEQPDYLDLKLAVADR	360		
Qy	361	VDIAKSEIENGDEVKSCDLBEVMVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR	420		
Db	361	VDIAKSEIENGDEVKSCDLBEVMVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR	420		
Qy	421	SVSRKSLPDLQKQEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLKDFLQDACRG	480		
Db	421	SVSRKSLPDLQKQEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLKDFLQDACRG	480		
Qy	481	FYQDGPGRDRAEAKGPAKPTGQKWLDDLQKSENPRDLFLMAVLQNRHEMATYFWAM	540		
Db	481	FYQDGPGRDRAEAKGPAKPTGQKWLDDLQKSENPRDLFLMAVLQNRHEMATYFWAM	540		
Qy	541	GQEGVAALAAACKILKEMSHLETEAARAATREAKYERLALDLFSECYNSNSEARAFALLV	600		
Db	541	GQEGVAALAAACKILKEMSHLETEAARAATREAKYERLALDLFSECYNSNSEARAFALLV	600		
Qy	601	RNRCSWKTTCIHLATEADAKAFAHGDGVQAFTRIWMGDMAAGTPIILRLGAFCLCPALV	660		
Db	601	RNRCSWKTTCIHLATEADAKAFAHGDGVQAFTRIWMGDMAAGTPIILRLGAFCLCPALV	660		
Qy	661	YTNLITPSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRPRAVFL	720		
Db	661	YTNLITPSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRPRAVFL	720		
Qy	721	LTRWRKFWGAPVTVPLGNVVMYFAFLFTYTVLLVDFRPPQPGSGPEVTLYFWVFTVLV	780		
Db	721	LTRWRKFWGAPVTVPLGNVVMYFAFLFTYTVLLVDFRPPQPGSGPEVTLYFWVFTVLV	780		
Qy	781	BEIRQGFPTDDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTVLAM	840		
Db	781	BEIRQGFPTDDETHLVKKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAFEAGRTVLAM	840		
Qy	841	DFMVFTLRILHIFAIHKQLGPKIIVVERM	869		
Db	841	DFMVFTLRILHIFAIHKQLGPKIIVVERM	869		

Search completed: June 22, 2005, 18:15:39
Job time : 184 secs

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OM protein - protein search, using sw model

Run on: June 22, 2005, 18:09:49 ; Search time 45 Seconds
(without alignments)
1932.581 Million cell updates/sec

Title: US-09-834-792D-4
Perfect score: 6093
Sequence: 1 MQDVQGPFGSGDAEDRE.....HRGGLDGWEPGAGQPPSDDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6093	100.0	1165	4	US-09-949-016-6874
2	6085	99.9	1165	4	US-09-949-016-11392
3	2040	33.5	1529	4	US-09-949-016-11100
4	2039	33.5	1503	4	US-09-600-087-2
5	2039	33.5	1503	4	US-09-949-016-6341
6	1566.5	25.7	1095	3	US-09-112-096-15
7	1566.5	25.7	1095	4	US-09-636-215-778
8	1566.5	25.7	1095	4	US-09-685-166A-778
9	1566.5	25.7	1095	4	US-09-679-426-778
10	1566.5	25.7	1095	4	US-09-759-143-778
11	1566.5	25.7	1095	4	US-09-651-236-778
12	1558.5	25.6	1095	4	US-09-636-215-780
13	1558.5	25.6	1095	4	US-09-685-166A-780
14	1558.5	25.6	1095	4	US-09-679-426-780
15	1558.5	25.6	1095	4	US-09-759-143-780
16	1558.5	25.6	1095	4	US-09-651-236-780
17	1240.5	20.4	1533	1	US-08-623-679-9
18	1240.5	20.4	1533	3	US-08-933-774-9
19	1240.5	20.4	1533	3	US-09-181-030-9
20	1240.5	20.4	1533	3	US-09-534-242-9
21	1240.5	20.4	1533	3	US-09-454-854-9
22	1240.5	20.4	1533	3	US-09-164-671-9
23	1240.5	20.4	1533	4	US-09-182-113-9
24	1240.5	20.4	1533	4	US-08-862-442-9
25	1162.5	19.1	1497	1	US-08-623-679-7
26	1162.5	19.1	1497	3	US-08-933-774-7
27	1162.5	19.1	1497	3	US-09-181-030-7

28	1162.5	19.1	1497	3	US-09-534-242-7	Sequence 7, Appli
29	1162.5	19.1	1497	3	US-09-454-854-7	Sequence 7, Appli
30	1162.5	19.1	1497	3	US-09-164-671-7	Sequence 7, Appli
31	1162.5	19.1	1497	4	US-09-182-113-7	Sequence 7, Appli
32	1162.5	19.1	1497	4	US-08-862-442-7	Sequence 7, Appli
33	820	13.5	315	3	US-09-020-956-112	Sequence 112, App
34	820	13.5	315	3	US-09-030-607-112	Sequence 112, App
35	820	13.5	315	3	US-09-439-313-112	Sequence 112, App
36	820	13.5	315	3	US-09-352-616A-112	Sequence 112, App
37	820	13.5	315	4	US-09-232-149A-112	Sequence 112, App
38	820	13.5	315	4	US-09-159-812-112	Sequence 112, App
39	820	13.5	315	4	US-09-636-215-112	Sequence 112, App
40	820	13.5	315	4	US-09-685-166A-112	Sequence 112, App
41	820	13.5	315	4	US-09-115-453-112	Sequence 112, App
42	820	13.5	315	4	US-09-688-489-112	Sequence 112, App
43	820	13.5	315	4	US-09-679-426-112	Sequence 112, App
44	820	13.5	315	4	US-09-759-143-112	Sequence 112, App
45	820	13.5	315	4	US-09-651-236-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-09-949-016-6874
; Sequence 6874, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6874
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6874

Query Match	100.0%;	Score 6093;	DB 4;	Length 1165;
Best Local Similarity	100.0%;	Pred. No. 0;		
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QY	1	MODVQGPFGSGDAEDRELGHRGEVNFVGGSGKKRKFVVRVPSGVAPSVLFDLLAEW	60	
Db	1	MODVQGPFGSGDAEDRELGHRGEVNFVGGSGKKRKFVVRVPSGVAPSVLFDLLAEW	60	
QY	61	HLPAFNLVSVLGEEROPFAMKSLRDVLRKGLVKAQSGMTLTSALRGLARHVQAV	120	
Db	61	HLPAFNLVSVLGEEROPFAMKSLRDVLRKGLVKAQSGMTLTSALRGLARHVQAV	120	
QY	121	RHSLASTSTKRVVAVGASLGRVLRHRIEAEQDFPVHPEDDGGSGGGLCSLDSNL	180	
Db	121	RHSLASTSTKRVVAVGASLGRVLRHRIEAEQDFPVHPEDDGGSGGGLCSLDSNL	180	
QY	181	SHFILVEPPGPKGDLTELRLRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTERI	240	
Db	181	SHFILVEPPGPKGDLTELRLRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTERI	240	
QY	241	SRAVEQAAPWLILVGGGIADVLALVNQPHLLVPKVAEQKFKPSKHFSWEDIVRWT	300	
Db	241	SRAVEQAAPWLILVGGGIADVLALVNQPHLLVPKVAEQKFKPSKHFSWEDIVRWT	300	
QY	301	KLQNITSHQHLITVYDFEGSGEELDTVLKALVKACKSHSQBPQDYLDELKLAWADR	360	

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301 KLLQNTTSHQHLITVYDFEQQSGSELDITVILKALVKACKSHSQPQDYLDELKLA VADR 360
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361 VDIKASEIFNGDVWKSODLEVMVDALVSNKPFVRLFVDNGADVADFLTYGRLQELYR 420
421 SVSRKSLLLFDLQKQEBEARLTLAGLTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
421 SVSRKSLLLFDLQKQEBEARLTLAGLTQQAAREPPAGPPAFSLHEVSRVLKDFLQDACRG 480
481 FYQDGRPGDRRAEKGPAKRTGQKWLDDLNQKSENPMWDLFLMAVLQNRHEMATYFWAM 540
481 FYQDGRPGDRRAEKGPAKRTGQKWLDDLNQKSENPMWDLFLMAVLQNRHEMATYFWAM 540
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1081 TAHRVDFPTAKYLGRLREGEKIKLESQINVCVSVLVSSVADVLAQGGGPRSSQHCGBSQ 1140
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RESULT 2
US-09-949-016-11392
; Sequence 11392, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11392
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11392

Query Match          99.9%; Score 6085; DB 4; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQDVQGRPGSGDAEDRRRELGLHGRGVNFGSGGKKGKGFVRVPSGVAPSVLPDLLLAEW 60
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Db 361 VDIKASEIFNGDVWKSODLEVMVDALVSNKPFVRLFVDNGADVADFLTYGRLQELYR 420
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Qy 601 RNRCSKTTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPILRLLAGAFLCPALV 660
Db 601 RNRCSKTTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPILRLLAGAFLCPALV 660
Qy 661 YTNLITFSEAPLRTGLDQLDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRGPRAVFL 720
Db 661 YTNLITFSEAPLRTGLDQLDLSLDTSEKSPLYGLQSRVEELVEAPRAQDGRGPRAVFL 720
Qy 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYTVLLVDFRPPQSGSGPEVTLYFWVFTLV 780
Db 721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYTVLLVDFRPPQSGSGPEVTLYFWVFTLV 780
Qy 781 EEIRQGFPTDEDTHLVKFTLYVGDNNKCDMVAIFLIVGTCRMLPSPAFAEAGRTVLAM 840
Db 781 EEIRQGFPTDEDTHLVKFTLYVGDNNKCDMVAIFLIVGTCRMLPSPAFAEAGRTVLAM 840
Qy 841 DFMVFTLRLLIHI FAIHKQLGPKIIIVVERMMKDVFFLFFLSVNLVAYGVTQTALLHPHDG 900

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Db 841 DFMVFTLLRIHFAHKQGLGKFLIIVRMKMDVFFFLSVLVAAGVTTQALLPHDG 900
Qy 901 RLEWIFRVLRYPLQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLY 960
Db 901 RLEWIFRVLRYPLQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLY 960
Qy 961 TFLVTVNVLNLLIAMESTYFQVQGNADMFQFORNLIVEHERPALAPPTILLSHL 1020
Db 961 TFLVTVNVLNLLIAMESTYFQVQGNADMFQFORNLIVEHERPALAPPTILLSHL 1020
Qy 1021 SLTLRRVFKAEHREHLEHRLDPLDQKVVTWETQENFLSKMKRRRDSGEVLRK 1080
Db 1021 SLTLRRVFKAEHREHLEHRLDPLDQKVVTWETQENFLSKMKRRRDSGEVLRK 1080
Qy 1081 TAHRVDFIAKYLGLRQEKRIKLESQINVCVSVLVADVLAQGGGPRSSQHCQGSQ 1140
Db 1081 TAHRVDFIAKYLGLRQEKRIKLESQINVCVSVLVADVLAQGGGPRSSQHCQGSQ 1140
Qy 1141 LVAADHRCGLDGEQPGAGQPPSDT 1165
Db 1141 LVAADHRCGLDGEQPGAGQPPSDT 1165

RESULT 3

US-09-949-016-11100
; Sequence 11100, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11100
; LENGTH: 1529
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11100

Query Match 33.5%; Score 2040; DB 4; Length 1529;
Best Local Similarity 38.8%; Pred. No. 1.7e-190;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;
Qy 26 GEVFGSGKGRKFKVRVPSGVAPSVLFDLLAEHLPAPNLVSLVGBEQPFAMKSWLR 85
Db 154 GDIVFTGLSQVKVYRVVSQDTSSVYHLMTHQWGLDVPNLLISVYTGAKFNMPREK 213
Qy 86 DVLKGLVKAQSTGAWILTSALRVGLARHVGQAVRDHSLASTSTKRVVAVGMSLGRV 145
Db 214 SIFRGLVKVQTGAIIITGSGHTGMVKQVGEARDFSLSSYKEGELITIGVATWGTV 273
Qy 146 LHRRIIEAQEDPPVHYPEDDGGSQGPLCLSDNSHFLVIEPFGPKGDGLTELRLE 205
Db 274 HRREGLIHPGTSFPAEYILDEDG-QGNLTCLDSNHSFHLVDDGTGHQGVETPLRLLE 332
Qy 206 KHTSEQAGVGGTSTETPVLCLLVGDPNLTLEISRAVEQAAPWILVSGSGIADVLA 265
Db 333 KFISEQTKERGGV-AKIPICVVLVEGGPGTLTINATNGTFCVVVEGSRVADVIAQ 391
Qy 266 LVNQP--HLVVPKVAEQ---FKEKFPKSHFSEWEDIVRMTKLLQNITSHOHLTVYDFEQ 320
Db 392 VANLPVSDITISLIQKLSVFFQEMFET--FTESRIVEWTKKIQDIVRRRQLLTVFREK 449

Qy 321 EGSELDVTILKALVACKSHSQEPQDYL-ELKLVANRVDIAKSEIFNGDVEWKSCD 379
Db 450 DGQDQDVDAIJLQALLKASRSQDHFHGWHDQKLAVANRVDIARSEIFMDEWQKPSD 509
Qy 380 LEEVWDVALVSNKPEFVRLFDGADVADFLTYGRLOELYSRSKSLIPDLLOKQBEA 439
Db 510 LHPTMTAALISNKEPFVKLFLENGVQLKEFVTWDTLLYENLDPSCLFHSKLOK----- 564
Qy 440 RLTLAGLGTQARPPAGP--PAFSLHEVSRVLKDFLDQACRGFYQDQGRDRR----- 492
Db 565 -----VLVEDPPEPACAPAPRLQMEHVAQVRLLELLDFTQPLYPRPHNDRLLLPV 618
Qy 493 -----AEKPAKRPCTQKWLLDLNQKSNPWRDLFLWAVLQNRHENATYFWAMQ 542
Db 619 PHVKLVNQGVSRLSRYKRSGHVTF-----TMDPIRDLTLIWAIVQNRRELAGIWAQSQ 672
Qy 543 EGVAALAAACKIKEMSHLETEAAR---ATREAKYERLALDLFSECSNSEARAFALL 599
Db 673 DCIAAALACSKIKELSKKEEDTDSSEMLALAB-EYEHRAIGVFTECYRDEERAQKLL 731
Qy 600 VRNRCSKTTCLHLATEADAKAFFAHDGVOAFTRIWWGDMAGTPIRLLLGAPLCPAL 659
Db 732 TRVSEANGKTTCLQALEAKDMKFSVHCGIQAFLTKVMWGLSVNDGLWRVTLCLAPPL 791
Qy 660 VYTNLITFSEEARPLRTGLELDLSDLTEKSPLYGLQSRVEELVEAPRAQDGRPRAVF 719
Db 792 LLTGLISPREKR-----LQD-----VGTFAA----- 812
Qy 720 LLTRWRKFWGAPVTVFLGNVVMYFAFLFTVYLLVDRPPPPQSGSGEVTLTYFWFTLV 779
Db 813 ---RARAFPTAPVVVFLNLSYFAFLCFAYVLMVDFQV---PSWCEAIYLMFSLV 866
Qy 780 LEETROGFTTDBDTHLVKKFTLYYGDNNKMDWAFIFIVGVTCTMLPSFAEAGRTVLA 839
Db 867 CEMRQLFYDDECCLMKKAALYFSDFWNKLDVGAILLVAGLTCLRLIPATLYPGRVILS 926
Qy 840 MDMVFTLRLIHFALHKLQKGIIVVERMMKDVFFFLFSLVWLVAAGVTTQALLPHD 899
Db 927 LDFILFCLRLMHIPTISKTGLPKIIIVKRMKDVFFFLFLLAVVVSFVAKQAIIHNE 986
Qy 900 GRLEWIFRVLRYPLQIFQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWLVILLY 948
Db 987 RRVDFRGLVAVVHSLYITFGQIPGIDGVNFPNHCSPNGTDPY----KPKCPESDATQ 1042
Qy 949 --LYANWLVILLVTFLLVTVNVLNLLIAMESTYFQVQGNADMFQFORNLIVEHER 1006
Db 1043 RPAFFEWLTLLCLLYLFTNILLNLLIAMESTYFQVQHTDQIWKFORHDLIEYHG 1102
Qy 1007 RPALAPPFILLSLTLRRVFKAEHREHLEHRLDPLDQKVVTWETQENFLSKM 1066
Db 1103 RPAAPPPFILLSHLQLFIKRVVLKTPAKRHKQKKNKLEKNEEAALLSWEIYLKENYLN 1162
Qy 1067 EKRRDSEGEVLRKTAHRVDFIAKYL-----GGLREQEKRIKLESQINVCVSVLVSS 1118
Db 1163 QFOQKORPEKTIEDISNKVDAMVDLLDPLKRSQSM-----EORLASLEEQAQTAQLAW 1219
Qy 1119 VADVLAQGGGPRSSQHCQGSQVLAAD---HRGGLDGEWQPG 1157
Db 1220 IVRTLRSAGSSEADVPTLASQAAAEEDPAEFGGRKTEEPG 1261

RESULT 4

US-09-600-087-2
; Sequence 2, Application US/09600087
; Patent No. 6548272
; GENERAL INFORMATION:
; APPLICANT: Shimizu, No. 6548272uyoshi
; APPLICANT: Nagamine, Kentaro
; TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN
; FILE REFERENCE: 11283-004001 US/09/600,087
; CURRENT APPLICATION NUMBER: 2000-07-11
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: PCT/JP99/06289

;; PRIOR FILING DATE: 1999-11-11
;; PRIOR APPLICATION NUMBER: JP/321200/1998
;; PRIOR FILING DATE: 1998-11-12
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 1503
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: TRANSMEM
;; LOCATION: (320)...(344)
;; NAME/KEY: TRANSMEM
;; LOCATION: (750)...(773)
;; NAME/KEY: TRANSMEM
;; LOCATION: (794)...(818)
;; NAME/KEY: TRANSMEM
;; LOCATION: (867)...(891)
;; NAME/KEY: TRANSMEM
;; LOCATION: (900)...(924)
;; NAME/KEY: TRANSMEM
;; LOCATION: (932)...(956)
;; NAME/KEY: TRANSMEM
;; LOCATION: (1024)...(1048)
US-09-600-087-2

Query Match 33.5%; Score 2039; DB 4; Length 1503;
Best Local Similarity 38.8%; Pred. No. 2.1e-190;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;
QY 26 GEVNFSGGKRGKRVVPSPGVAPSLFDLLAEWHLPAPNLVSLVSGEOPFAMKSWLR 85
DB 128 GDIVFTGLSQKVKYVRVSDTPSSVIYHMTQHWGLDVPNLLISVTGAKNFNKPRLK 187
QY 86 DVLRLGLVKAQSTGAWILTSALRVGLARHVGQAQRDHSLSASTSTKRVVAVGMSLGRV 145
DB 188 SIFRGLVKVAQTGAWITGGSHVGMVKMGVGEAVRDFSLSSSYKEGELITIGVATWGTV 247
QY 146 LHRRLLEBAQEDFPVHYPPDDGGSCPLSDLSNLSHPILVEPGRPDPGKDGGLTELRLLE 205
DB 248 HRREGLIHTGSPFAEYILDEG-QGNLTCLDSNHSFILVDDGHGQYGVIEPIRLTLE 306
QY 206 KHISQRAGYGTGSIPIVLCLLVNGDPNLTISRVAEQAAPMLILVSGSGIADVLAA 265
DB 307 KFISEQTGERGV-AIKPIVCVVLGEGGPGTLHTIDNATTGTPCVVVGSGRVADVIAQ 365
QY 266 LVNQP--HLLVPKVAEQ--FKEKPSKSHSWEDIVRWTKLQNIHQHLLTVYDPEQ 320
DB 366 VANLPVSDITSLIQKLSVFFQEMFET--FTESRIVEWTKIQDIVRRRLQTLVPRGK 423
QY 321 EGSEBELDTVILKALVKACKSHSQBPQDYLD-ELKLAVANDRVDIAKSEIFNGDVEMKSCD 379
DB 424 DQQQDVDAIILQALLKASRSQDHGHEWHDQLKLVANWNRVDIARSEIFMDEWQWPKSD 483
QY 380 LEEVVDVALVNGKEFEVRLFDVNGADVADFTYGRQLQELYSVRKSLFDLLQKQEEA 439
DB 484 LHPTMTAALISNKEFEVRLFDVNGADVADFTYGRQLQELYSVRKSLFDLLQKQEEA 538
QY 440 RLTLAGLTQARPPAGP--PAPSLHEVSVLKDPLQDACRGYQDGRGDRRR----- 492
DB 539 -----VLVEDPERPACAPAPRIQMHVAVQLRELLGDFTPQLYPRPRINDRLRLLPV 592
QY 493 -----AEKGPAPKPTQKQLLDLQNKSEPNRDLFLWAVLQNRHEMATYFWAMQ 542
DB 593 PHVKLVNGVSLRSLYKSSGHVTF-----TMDPIRDLIIAIVQNRRELIGIWAQSQ 646
QY 543 EGVAALAAACILKEMSHLETAAR---ATRAKYERIALDLFSSCYNSSEARAPALL 599
DB 647 DCIAAALACSKILKELKEEDTDSSEMLALAE-EYEHRAIGVFTCYRKEDEARAQKLL 705
QY 600 VRRNRCKSTTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAGTPIRLILGAFGLCPAL 659
DB 706 TRUSEANGKTICLQALEAKDMKVSHGIGTQAFITKVVWGQLSVNDGLWRVTLICMLAPPL 765

QY 660 VYTNLIITSEAPRLTGLELDQLDLSLDEKSPLYGLQSRVEELVEAPRAGQGRPRAVF 719
DB 766 LLTGLISFREKR-----LQD-----VGTAA----- 786
QY 720 LLTRWRKFWGAPVTPLGNVVMYFAFLFTYVLLVDPRPPQGPSPGSEVTLIYFWVTIV 779
DB 787 ---RARAFPTAPVVVPHNLISYFAFLCLFAYVLMWDFQV---PSMCECAIYLMWLSLV 840
QY 780 LEEIRQGFDEDETHLVKFKETLYVGDNNKCDMVAIEFLTVGVTCRMLPSAFEAGRTVLA 839
DB 841 CEEMRQLFYDPDECGLMKKAAALYFDFWNLKLDVCAILLFVAGLTCRLIPATLIPGRVILS 900
QY 840 MDMVFTLRILHPIAHKQLGPKIIVVERMKOVFFFLFSLVWLVAIVGTQTALLPHD 899
DB 901 LDFILFCLRLMHIFTISKTLPKIIIVKRWKDVFFFLFLLAVWVSGVAKAILIHNE 960
QY 900 GRLEWIFRRVLYREYLOIFQIP--LDEIDEARVNC--THPLLEDSDSPSCPS----- 948
DB 961 RRVNLFGRGAVYHSYLTIFQIPIGYIDVNFNPEHCSPNGTDPY---KPKCPESDATQQ 1016
QY 949 --LYANWLVIALLVTFLLVNTNLLIMNLLIAMFSYTFVQVQGNADMFWKFORYNLIVEYHE 1006
DB 1017 RPAFPEWLTULLCLLYLFTNILLNLLIAMFNYYTQQVQEHDDQIKWFORHDLIEBYHG 1076
QY 1007 RPALAPPFILLSHLSLTLRRVFKKEAHEKHEHLERDLPDLPDOKVVTWTVQKFNFLSKM 1066
DB 1077 RPAAPPPFILLSHLQLFKRVVLKTPAKRHKQLKNKLENEEAALLSWEYLYKENYLNQR 1136
QY 1067 EKERRDSEGVLRKTAHRVDVFIAYL-----GGLEOEKRIKCLSEQINCYCSVLVS 1118
DB 1137 QFOQKQRPQEKIEDISKNVDAMVDLDDLPKSGSM---EQRLASLEEQVAQTARALHW 1193
QY 1119 VADVLAQGGGPRSSQHGEGSLVAAD---HRGGLDGWEQPG 1157
DB 1194 IVRTLASGFSSEADVPTLASQKAEPEDAEPDGPGRKKTBEFG 1235
RESULT 5
US-09-949-016-6341
; Sequence 6341, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCES: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6341
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6341

Query Match 33.5%; Score 2039; DB 4; Length 1503;
Best Local Similarity 38.8%; Pred. No. 2.1e-190;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;
QY 26 GEVNFSGGKRGKRVVPSPGVAPSLFDLLAEWHLPAPNLVSLVSGEOPFAMKSWLR 85
DB 128 GDIVFTGLSQKVKYVRVSDTPSSVIYHMTQHWGLDVPNLLISVTGAKNFNKPRLK 187
QY 86 DVLRLGLVKAQSTGAWILTSALRVGLARHVGQAQRDHSLSASTSTKRVVAVGMSLGRV 145

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188 SIFRGLVKVAQTTCGAWIITGSGHTGMVKQGEAVRDFSLSSYKEGELITIGVATGCTV 247
146 LHRRILEAEQEDFPVHYEDDGGSCPLCSLDSNLSHFIYEPGPGKDGTELRLRL 205
248 HRREGLIHPTGSPFAEYILDEG-QCNLTCLDSNHSFILVDGTHGQYGVPIURTRLE 306
206 KHISORAGYGTGIEIPVLCVLLVNGDPNTERISRAVEQAAPMLIIVGSGGIADVLAA 265
307 KFISQTKERGQV-AIKPIVCVILEGGGTHTTIDNATTNGTGPCVVEGSGSRVADVIAQ 365
266 LVNQP--HLLVPKVAEKQ---FKKFPSPKHSWEDIVRWTKLLQNTSHQHLITVYDEQ 320
366 VANLPVSDITISLIQKLSVFQEMFET--FTESRIVEWTKKIQIDVRRRQLITVREGK 423
321 EGSEELDTVILKALVKAKSHSQEPQDYLD-ELKLAWANDRVDIKAKSEIFNGDVEMKSCD 379
424 DQOQDVDAILOALLKASRSODFHGENWDHQLKLAWAMNRVDIARSEIFMDEWQKPSD 483
380 LEEVMDALVSNKPEFVRVLPVNGADVADFLTYGRLOELYSVRSKSLFDLLQKQBEA 439
484 LHPTTAAALISNKPFEVFLNGVQKFEVTDWTLTYLYENLDPSCFLSHKLOK----- 538
440 RLTLAGLGTQOAREPPAGP--PAFSLHYSRVLKDFLODACRGFYODGPGDRRR----- 492
539 -----VLVEDPERPACAPAPLQMHVAQVLRLLGDFTOPLYPXPRHNDRLRLLPV 592
493 -----AEKGPAPKRTGQKWLIDLKQENPWRDLFLWAVLONRHEMATYFWAMQO 542
593 PHVKLVNQVSLRSYKRSRGHVTF-----TMDPIRDLIIWAIQVNRRELAGIWAQSQ 646
543 EGVAAALACKILKEMSHLETEAAR---ATREAKYERLALDLFSECYNSGEARAFALL 599
647 DCTAALACSKILKELUSKEEDTDSSEMLALAE-EYEHRAIGVFTECRKDEERAQKLL 705
600 VRNRCSWTKTCLHATEADAKAFFADHGVAQFLTRIMWGMMAAGTPILRLGAFICPAL 659
706 TRVSEANGTKTCLQALEAKMKFVSHGGIQAFLTKVMWGSLVDNGLWRVTLCLMAFPL 765
660 VYTNLITFSEAPLRTGLELDQLDLSLTEKSPLYGLQSRVELVAPRAQDGRPAVF 719
766 LTLGLISFREKR-----LQD-----VGTCAA----- 786
720 LLTRWKFAGPVTYFLGNVVMYFAFLFTYVLLVDPRPPGSGPEVLYFWVFTLV 779
787 ---RARAFFTAPVYFHLNLTYSFAELCLFAYILMVDQPV---PSWCECAIYMLFSLV 840
780 LEEIROGFFTDETHLVKFTLVVGNWKNCDMVAFPLFTVGVTCRLPSAFAGRTVLA 839
841 CEEMROLYDPDCEGLMKKAAALFSDFWNKLDVGAILLFVAGLTCLRLIPATLYPGRVILS 900
840 MDPWVFTLRILIHFAIHKQGPKIIIVVERMMKDVFFELFSLVWLVAYGVTTOALLPHPD 899
901 LDFILFCLRLMHFTISKTLGPKIIIVKRMKDVFFELFLLAVVWSFGVAKQAILIHE 960
900 GRLEWIFRVRVLYPOIGQIP--LDEIBARVNCs---THPLLLEDSPSCPS----- 948
961 RRVDWLPFGAVYHSLYITFGQIPGYIDGVNFNPEHCSPNGTDPY-----KPKCESDATQO 1016
949 --LYANWLVTLITVTLNVLNMLLIAMFSYTFQVQGNADMFWKFORNYLIVSYHE 1006
1017 RPAPEPEWTLVLLCLYLFTNLINLLIAMFNITFOQVEHTDOIWKFORHDLIEYHG 1076
1007 RPALAPFPFLLSHLSLTLRRVFKKEAEKREHLERDLPDLDQKVVVTWVQENFLSKM 1066
1077 RPAAPFPFLLSHLQLFKRVVLTAPKRRHQLKLEKNEEAALLSWEIYKENVLQNR 1136
1067 EKRDRSEGEVLRTAHRVDPIAKYL-----GGLREQKR1KCLSEINCYNSVLVSS 1118
1137 QFOQKORPEQKIEDISNKVDAMVDLLDLDPLKRSISM---EORLASLEEQAQTARALHW 1193
1119 VADVLAQGGGPRSSOHCCEGSQLVAD---HRGGLDGWEQPG 1157
1194 IVTRLASGFGSEADVPVTLASQKAAEBEPDAPFGGRKKTTEPG 1235

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RESULT 6

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US-09-112-096-15
; Sequence 15, Application US/09112096
; Patent No. 6194152
; GENERAL INFORMATION:
; APPLICANT: Reiner Laus
; APPLICANT: Michael H. Shapiro
; APPLICANT: Larisa Tsavaler
; TITLE OF INVENTION: Prostate Tumor Polynucleotide and
; TITLE OF INVENTION: Antigen Compositions
; FILE REFERENCE: 7636-0015.30
; CURRENT APPLICATION NUMBER: US/09/112.096
; EARLIER FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: 60/056.110
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-112-096-15

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Query Match      25.7%; Score 1566.5; DB 3; Length 1095;
Best Local Similarity 34.3%; Pred. No. 3.9e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

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QY 26 GEVPPGGGKRGKVRVPSPGVAFLFDLLAEWHLPAPNLVSLVSGEPPFAMKSLR 85
DB 95 GDIPETLGGK-GKTYRLSCDTDAFELYELLTQHWHLLTPNLVLSVTGAKNFALKPRMR 153
QY 86 DVLKGLVAKAQTGAWILTSALRYGLARHVGQAVRHSLASTSTKVRVAVGMAASLGRV 145
DB 154 KIFSR-LYIAQSKGAWILTGTHYGLTKYIGEVVRDNTI-SRSEENIIVAGIAANGV 211
QY 146 LHRRILE---EAQEDFPVHYEDDGGSCPLCSLDSNLSHFIYEPGPGKDGTELRL 202
DB 212 SNRDTLRNCDAEGYFLAQLMDD--FTRDPLVILONNTHLLVDNGCHGHTVEAKLRN 270
QY 203 RLEKHISE---QRAQYGGTSGTSEIIPVLCVLLVNGDPNTERISRAVEQAAPMLIIVGSGGI 259
DB 271 QLEKHISERTIQDSNYG---KIPVCPAQGGKGTLLKAINTSIKNKIPCVVVEGSGRI 326
QY 260 ADVLAALVNPQLLVPKVAEKFKKFPSS--KHFSWEDIVRWTLLQNTSHQHLITVYD 317
DB 327 ADVIASLVEVEDAPTSSAVKEKLVRFPLPRTVSRLESEETESIKWLKEILCSHLLTVIK 386
QY 318 FQEGSEELDTVILKALVKAKSHSQEPQDYLDLDELKLAWANDRVDIKAKSEIFNGDVEMK 377
DB 387 MEEAGDEIVSNALISVALYKAFSTSQDKDNWNGQLKLLLEWNLQDLANDEIFTNDRMES 446
QY 378 CDLEEVMDALVSNKPEFVRVLPVNGADVADFLTYGRLOELYSVRSKSLFDLLQ---R 434
DB 447 ADLQEVWFTALIKDRPKFVRLFLEGNLNRKELTDLVLTFLF--SNHFTSLVVRNLQIAKN 505
QY 435 KOEAEARLTLAGLTQOAREPPAGPAPFSLHYSRVLKDFLODACRGFYODGPRG--DRRRA 493
DB 506 SYNDALLTF-----VWKLVAEFR-----RGFRKEDRNGRDEMID 539
QY 494 EKGPAKRPCTQKWLIDLKQENPWRDLFLWAVLONRHEMATYFWAMQOEGVAAALAAACK 553
DB 540 E-----LHDVSPITRHPLQALFIWAILQNKLSKVIVWQTRCTGLTAAALGASK 587
QY 554 ILKEMSHLETEAARATREA--KYERLALDLFSECYNSGEARAFALLVRNRNCWKTTC 611
DB 588 LKTLAKVKNIDINAAGESEELANEYETRAVELFTECYSSDEDLAEQLLVYSCWAGGSGNC 647
QY 612 LHATLAEADAKAFPAHDGVAQFLTRIMWGMMAAGTPILRLGAFICPALCVNLITVSEEA 671
DB 648 LELAVEATDQHTAQPGVQNFSLSKQWYGEISRDTKNWKIILCLFIPLVCGGFGVFRKK- 706

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QY 672 PLRTGLEDLQDLSLDTSEKSPYGLQSRVEELVEAPRAQDGRPAVFLTRWRKFWGAP 731
Db 707 -----PVDKHK-----LLWYVAFFTSP 725
QY 732 VTVFLGNVMYFAFLFTYVLLVDFRPPPGQSPGPEVTLYFWVFTLVLEIRQGFPTDE 791
Db 726 FVVFSSNVVFIYAFLLFAYLLMDFHSVPH---PPELVLSLVFLVFCDEVQWYNGV 782
QY 792 DTHLVKKTLYVGDNNKCDMAVFLFVIGVTCRM---LPSAFAGRTVLAMDPMVFTLR 848
Db 783 N-----YFTDLNVMVMDTGLFYFTAGVFRHLHSSNKSLSYSGRVIFCLDYIIFTLR 833
QY 849 LIHIFAIHQGLPKIIVVERMMKDVFFFLFSLVNLVAYGVTTQALLPHDGRLEWIFRR 908
Db 834 LIHIFVSRNLGPKIIMLQMLIDVFFFLFVAVMWVAFGVARQGLRQNEQRWIFRS 893
QY 909 VLYRPYLQIPGQIPDEIDEAR---VNC-----THPLLE-DSPSCPSLYANWLVL 959
Db 894 VIVEPYLAMFGQVPSD-VDGTTYDFAHCTFTGNEKPLCVLDEHNLPR-PPWITITPLV 951
QY 960 VTELLVNTVLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPFFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTVOENNDQVWKFORYNLIVEYHERPALAPFFILLSH 1011
QY 1020 LSLTLRRVFKKEAHEKREHLERDLPDLDQKVVTWETVOKENFSLKMEKRRDSEGEVLR 1079
Db 1012 FYMVVKCFKCCCKEKNMESSVCCFKNEDNETLAWGVKKNYLVKINTKANDT-SEEMR 1070
QY 1080 KTAHRVDFIAKYLGG-LRQEKRIK 1103
Db 1071 HRFRQLDTKLANDKGLLKEIANIK 1095
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RESULT 7

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US-09-636-215-778
; Sequence 778, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636.215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 778
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-778
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Query Match 25.7%; Score 1566.5; DB 4; Length 1095;
Best Local Similarity 34.3%; Pred. No. 3.9e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;
QY 26 GEVNFSGSGKKGKGFVRVPSGVAFLFDLLAEWHLPAPNLVSLVSGSPFAMKSWLR 85
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Db 95 GDQFETLGKK-KGYIRLSCTDABEILYELLTQWHHLKTNLVISVTVGGAKNFALKRMR 153
QY 86 DVLRKGLVKAQSTGAWILTSALRVGLARHVGAQRDHSLASTSTKRVVVAVGMAISGRV 145
Db 154 KIPSR-LIYIAQSKGAWILGTGTHYGLTKYIGVVRDNTI-SRSSEENIYVAGIAAGMV 211
QY 146 LHRRIE---BAQEDFPVHYPEDDGGSGQGLCSLSDSNLSHFILVPEPQPGKGLTBLRL 202
Db 212 SNRDTLNRNCDAEGYFLAQYLMDD-FTRDPYILDNHHTHLLVDNGCHGHTPEAKLRN 270
QY 203 RLEKHISE---ORAGYGGTGSIEIPVLCILVNGDPNTERISRAVEQAAAPMLILVSGGI 259
Db 271 QLEKHISERTIQSNYGG---KIPVCPAQQGKETLKAINTSIKNKIPCVVVEGSGRI 326
QY 260 ADVLAALVNOPHLLVPKVAEKQFKPPS---KHFSWEDIVRWTKLLQNITSHQHLTYVD 317
Db 327 ADVIASLVEDEAPTSSAVKEKLVRLPRTVSRLSSEETESWIKLKEILCSHLLTVIK 386
QY 318 FEQSGSELDTVILKALVKACKSHSQBPQDYLDELKLAVDNRVDIAKSEIFNGDVEWKS 377
Db 387 MEEAGDEIVSNALSYALYKAFSTSEQDKNNMGQLKLLLEWNLQDLANDEIFTNDREWES 446
QY 378 CDLEEVNVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYRSVSRKSLFDLLQ--R 434
Db 447 ADLQEVWFTALIKDRPKFVRLFLEGLNLAKRKLTHDVLTELF-SNHFSTLVYRNLOAKN 505
QY 435 KQBEARLTLAGLTQQAAREPPGAPFAPSLHVSRLVKDFLODACRGYQDGRPG-DRRRA 493
Db 506 SYNDALLTF-----VNLVANPR---RGPRKEDNRGDEMDI 539
QY 494 EKGPAKPTQCKWLLDLNOKSENPRDPLFWAVLQNRHEMATYFWAQBGQGVAAALAAK 553
Db 540 E-----LHDVSPITRHPLOALFIWALQNKELSKVIMEQTRGCTTALAAGASK 587
QY 554 ILKEMSHLETEAABAARATREA---KYERLALDLFSECVSNSEARAFALLVVRNRCWSKTC 611
Db 588 LLKTLAKVKNIDINAAGESEBELANEYETRAVELTECYSSDEDLAQLLVYSCAWGSGNC 647
QY 612 LHLEADAKAFPAHDGVOAFLTRIWMGDMAAGTPILRLGLAFLCPALVVTNITFSEEA 671
Db 648 LELAVENTDQHTAQPGVQNFSLSKQWYGEISRDTKWKKILCLFIPLVCGGVSFRKK- 706
QY 672 PLRTGLEDLQDLSLDTSEKSPYGLQSRVEELVEAPRAQDGRPAVFLTRWRKFWGAP 731
Db 707 -----PVDKHK-----LLWYVAFFTSP 725
QY 732 VTVFLGNVMYFAFLFTYVLLVDFRPPPGQSPGPEVTLYFWVFTLVLEIRQGFPTDE 791
Db 726 FVVFSSNVVFIYAFLLFAYLLMDFHSVPH---PPELVLSLVFLVFCDEVQWYNGV 782
QY 792 DTHLVKKTLYVGDNNKCDMAVFLFVIGVTCRM---LPSAFAGRTVLAMDPMVFTLR 848
Db 783 N-----YFTDLNVMVMDTGLFYFTAGVFRHLHSSNKSLSYSGRVIFCLDYIIFTLR 833
QY 849 LIHIFAIHQGLPKIIVVERMMKDVFFFLFSLVNLVAYGVTTQALLPHDGRLEWIFRR 908
Db 834 LIHIFVSRNLGPKIIMLQMLIDVFFFLFVAVMWVAFGVARQGLRQNEQRWIFRS 893
QY 909 VLYRPYLQIPGQIPDEIDEAR---VNC-----THPLLE-DSPSCPSLYANWLVL 959
Db 894 VIVEPYLAMFGQVPSD-VDGTTYDFAHCTFTGNEKPLCVLDEHNLPR-PPWITITPLV 951
QY 960 VTELLVNTVLLMNLIIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPFFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTVOENNDQVWKFORYNLIVEYHERPALAPFFILLSH 1011
QY 1020 LSLTLRRVFKKEAHEKREHLERDLPDLDQKVVTWETVOKENFSLKMEKRRDSEGEVLR 1079
Db 1012 FYMVVKCFKCCCKEKNMESSVCCFKNEDNETLAWGVKKNYLVKINTKANDT-SEEMR 1070
QY 1080 KTAHRVDFIAKYLGG-LRQEKRIK 1103
Db 1071 HRFRQLDTKLANDKGLLKEIANIK 1095
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Db 1071 HRFRQLDTKLNLDKGLLKEIANKIK 1095

RESULT 8

US-09-685-166A-778

Sequence 778, Application US/09685166A

Patent No. 6630305

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darriek

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C21

CURRENT APPLICATION NUMBER: US/09/685,166A

NUMBER OF SEQ ID NOS: 898

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 778

LENGTH: 1095

TYPE: PRT

ORGANISM: Homo sapiens

US-09-685-166A-778

Query Match 25.7%; Score 1566.5; DB 4; Length 1095;

Best Local Similarity 34.3%; Pred. No. 3.9e-144;

Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

Qy 26 GEVFGGSKGKGFVRVPSGVAPSVLPDLLAEHLPAPNLVSVLSVGEOPFAMKSWLR 85

Db 95 GDIQFETLGGK-GKIRLSCTDDAEILYELLTQHWHLTPNLVSVISVGGAKNFALKPRWR 153

Qy 86 DVLRLGLVKAOSTGAWILTSALRVLGRHVQAVRDHSLASTSTKRVVAVGMASLGRV 145

Db 154 KIFSR-LIYIAOSKGNWILTTGGTHYGLTKYIGEVVRDNTI-SRSSEENIVAIGIAWGV 211

Qy 146 LHRRIE---EAQEDPPVHPYEDDGGSGPLSLDSNLSHFILVBPFGKDGGLTELRL 202

Db 212 SNRDTLRNCAEGYFLAQLMDD-PTRPFLYLDNNHLLVONGCHGCHPTVEAKLRN 270

Qy 203 RLEKHISE---QAGVGGTGSIEIPVCLLVNGDPNPLERISRAVEQAAPWLLVSGGI 259

Db 271 QLEKHISERTIODSNYGG---KIPIVCPAQGGGKETLKAINTSIKNKIPCVVVEGSGRI 326

Qy 260 ADVLAALVNQPHLLVPKVAEKOPKEKPPS--KHFSWEDIVRWTKLQNTISHQLLITVD 317

Db 327 ADVIASLVEVEDAPTSASVAKELVRLPRTVSRLSSEETESWIKWLKEILECSHLLTVIK 386

Qy 318 FEQSGSEELDTVLKALVKACKSHSQEPQDYLDLKLAVAWDRVDIAKSEIFNGDVEWKS 377

Db 387 MEEAGDEIVSNALSYALYKAFSTSEQDKNNWQGLKLLLEWNLQDLANDEIPTNDRWES 446

Qy 378 CDLEEVWVALVSNKEFEVRLFDVNGADVADFLTYGLYQLYLSVRSKSLPDLLO---R 434

Db 447 ADLQEVMTALIKDRPKFVRLFLNGLNLRKFLTHDVLTELF-SNHFTLVYRNLIQAKN 505

Qy 435 KQEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRVLKDLQDACRGFYQDGRPG-DRRRA 493

Db 506 SYNDALLTF-----VWKLVANFR-----RGRKEDRNGRDEMIDI 539

Qy 494 EKGPAPKPTGQKWLIDLNQKSENPRWDLFLWYVQNRHEMATYFWAMQBGVGAALAAACK 553

Db 540 E-----LHDVSPITRHPQLQALFWAILQNKELSKVITWQTRGCTTAAALGASK 587

Qy 554 ILKEMSHLETEAARATREA--KYERLALDLSSECYNSSEARAFALLVNRNRCWSKTTTC 611

Db 588 LLKTLAKVNDINAAAGESEELANEYETRAVELFTECYSSDEDELAQLLVVSCAENGSGNC 647

Qy 612 LHLATEADAKAFFAHGDVQAFLTRIWMGDMAAGPILRLGCAFLCPALVTVNTLITFSEE 671

Db 648 LELAVEATDQFTAPQGVQNFSLKQWYGEISRDTKWKKIILCLFIIPLVGCGFVSFRKK- 706

Qy 672 PLRTGLEDLQDLSDLTETKSPLYGLQSRVBEVAPRAOQGRGPRAVFLVTRMKFKWGP 731

Db 707 -----PVDKHKK-----LLWYVVAFTSP 725

Qy 732 VTVPGLNVVYFAFLFTVYLLVDRPPPGSGSPVTLVFWVFTLVLEIIRGGEFTDE 791

Db 726 FVFSMNWVYFAFLFLLFAVLLMDFHSVPH---PPELVLYSLVFLVFCDEVRQWYNGV 782

Qy 792 DTHLVKKTLYVGNWKNKCDMVAIFLFIIVGTCRM---LPSAFBAGRTVLAMDPMVFTLR 848

Db 783 N-----YFTDLNWNMDTLGLFYFIAGIVFRLHSSNKSLSYSGRVIFCLDIIFTLR 833

Qy 849 LIHIFAIHKOLGPKIIVVERMKDVFFFLFPLSVMLVAYGVTTQALLHPHDPGRLEWIFRR 908

Db 834 LIHIFTVSRNLGPKIIMLQRMILIDVFFFLFLFAVWVAFVQARQGLLRQNRWRWIFRS 893

Qy 909 VLYRPYLIQFQIPLDEIDEAR-----VNCS-----THPLLE-DSFSCPSLYANWLVILL 959

Db 894 VLYRPYLAQFQVPSD-VDGTTYDFAHCTFTGNSKPLCVLDEHNLPR-FPEWITPLV 951

Qy 960 VTFLLVNTVLLMLLIAMESYTFQVQGNADMFKFORYNLIVYHERPALAPPILLSH 1019

Db 952 CIYMLSTNILLVNLVAMFGYTVGTQENNDQVWKFQRYFLVQVYCSRLNIPFFPIVAY 1011

Qy 1020 LSLTRVRFVKEAEHREHLERDLDPDLDQKVVTVWETVQENFLSKMEKRDRDSGEVLR 1079

Db 1012 FYMVVKCKFCCKCKEKNMSESVCCFKEDNETLAWGVWKNYLKINTKANDT-SEEMR 1070

Qy 1080 KTAHRVDPIAKYLG-LREQEKRIK 1103

Db 1071 HRFRQLDTKLNLDKGLLKEIANKIK 1095

RESULT 9

US-09-679-426-778

Sequence 778, Application US/09679426

Patent No. 6759515

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darriek

APPLICANT: Li, Samuel

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C20

CURRENT APPLICATION NUMBER: US/09/679,426

CURRENT FILING DATE: 2000-10-02

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; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 778
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-679-426-778

Query Match      25.7%; Score 1566.5; DB 4; Length 1095;
Best Local Similarity 34.3%; Pred. No. 3.9e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

QY 26 GVNFGSGKRGKRVVPVSGVAPSVLPDLLAEWHLPAPNLVSVLVEEQPFAMKSWLR 85
Db 95 GDIQFETLGGK-GKYIRLSCDTEAEILYELLTQHWHLKTPLNLVSVTGGAKNFALKPRMR 153
QY 86 DVLKGLVKAQSTGAWILTSALRVGLARHVQAVRDHSLASTSTKVRVAVGMSLGRV 145
Db 154 KIFSR-LIYIAQSGKAWILTGTHYGLTKYIGEVVRDNTI-SRSSEENIValGIAAGMV 211
QY 146 LHRRIE---BAQDFPVHYVEDDGGSGPLCSLDSNLSHFILVEPQPKGDGLTELRL 202
Db 212 SNRDTLRNCDAEGYFLAQYLMDD-FTREDPLYLDNNHLLVNDGCHGHPVTEAKLRN 270
QY 203 RLEKHISE---ORAGYGGTSGSIEIPVLCVINGDPNPTLERISRAVEQAAPMLILVSGGI 259
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QY 260 ADVLAAVLNQPILLVPKVAEKQKKEFPS--KHFSWEDIVRWTKLQNTSHQHLTYVD 317
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QY 318 FEQSGSELDTVILKALVKAACKSHSQBPQDYLDELKLAVDWRVDIAKSEIFNGDVEKKS 377
Db 387 MEEAGDEIVSNATSYALYKAFSTSEQDKDNWNGQLKLLWNLQDLANDLFTNDRRES 446
QY 378 CDLEEVVMDALVGNKPEFVRLVDNGADVADLTTCRLOELYSRVSRSKSLDFDLQ---R 434
Db 447 ADLQEVMTALIKDRPKFVRLFLNGLNLRKFLTDHVLTELF-SNHFTLVYRNLIQAKN 505
QY 435 KQEBALTLGLGTQOARBPAGPPAFSLIHSYRVLKDFLODACRGFYQDGRPG-DRRA 493
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Db 540 E-----LHDVSPITRHPLOALFTWAILQNKKELSKVIWEQTRGCTLAALGASK 587
QY 554 ILKEMSHLETEAARATREA--KYERLALDLFGSCYSNSARAFALLVRNRCSWKTTC 611
Db 588 LLKTLAKVNDINAAGESEELANEYETRAVELFTECYSSDEDLAEQLLVYSCAANGSNC 647
QY 612 LHLATEADAKAFPAHDGVQAFTRIWGDMAGTPILRLIGAFICPALVYTNLITFSEA 671
Db 648 LLEAVEATDQHTAQPGVQNFSLSKQWYGEISRDTKNWKIILCLFIPLVCGFVSRKK- 706
QY 672 PLRTGLEDLQDLSLDTKSPLYGLQSRVLELVEAPRAQDGRPAVFLTRKRWKFWGAP 731
Db 707 -----PVDKHK-----LWYVVAFTSP 725
QY 732 VTFVGNVMYFAFLFTFYVLLVDPRPPGPGSPBVTLYFWVFTLVEEIRQGFTE 791
Db 726 FVFSWNVVFIATFLLFAYVLLMDHFSVPH---PPELVLSLVFLVFLFCDEVQWVNGV 782
QY 792 DTHLVKFKFTLVYGNMNMKDMVAIFLIVGTCRM---LPSAEAGRTVLAMDPMVFTLR 848
Db 783 N-----YFTDLNMVMDTLGLFYIAGIVFRLHSSNKSLSYGRVIFCDYIIFTLR 833
QY 849 LIHIFATHKOLGPKIIIVVERMKDVPFFFLSVLVAIVGVTQTALLPHDGRLEWIFRR 908
Db 834 LIHFTVSRNLGPKIIMLQGLDVFVFLFLFAVMVAFVARQGLLRQNEQRWEIFRS 893
QY 909 VLVRPYLQIFQIPLDIDEAR---VNCS-----THPLLEL-DSRSCPSLYANWLILL 959

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Db 894 VIYEPYLAAMFGQVPSD-VDGTTYDPAHCTFTGNESKPLCVELDEHNLP-R-FPEWITPLV 951
QY 960 VTFFLLVTVNLLNLLIAMFSYTFQVQGNADMFKFORYNLIVYHERPALAPFFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTQBNNDQVWKFQRYFLVQYCSRLNIPFPFIVFAY 1011
QY 1020 LSLTLRRVFKBAHKEHLEHLELDLPDLQKVVTWVQENFLSKMEKRRRSEGEVLR 1079
Db 1012 FYMVVKKCFKCCCKEKQMESSVCCFKNEDNETLAWGWMKENYLVKINTKANDT-SEEMR 1070
QY 1080 KTAHRVDFIAKVLGG-LREQEKRIK 1103
Db 1071 HRFQLDTKLNLDKGLKEIANKIK 1095

RESULT 10
US-09-759-143-778
; Sequence 778, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 778
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-778

Query Match      25.7%; Score 1566.5; DB 4; Length 1095;
Best Local Similarity 34.3%; Pred. No. 3.9e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

QY 26 GVNFGSGKRGKRVVPVSGVAPSVLPDLLAEWHLPAPNLVSVLVEEQPFAMKSWLR 85
Db 95 GDIQFETLGGK-GKYIRLSCDTEAEILYELLTQHWHLKTPLNLVSVTGGAKNFALKPRMR 153
QY 86 DVLKGLVKAQSTGAWILTSALRVGLARHVQAVRDHSLASTSTKVRVAVGMSLGRV 145
Db 154 KIFSR-LIYIAQSGKAWILTGTHYGLTKYIGEVVRDNTI-SRSSEENIValGIAAGMV 211
QY 146 LHRRIE---BAQDFPVHYVEDDGGSGPLCSLDSNLSHFILVEPQPKGDGLTELRL 202
Db 212 SNRDTLRNCDAEGYFLAQYLMDD-FTREDPLYLDNNHLLVNDGCHGHPVTEAKLRN 270
QY 203 RLEKHISE---ORAGYGGTSGSIEIPVLCVINGDPNPTLERISRAVEQAAPMLILVSGGI 259
Db 271 QLEKHISERTIODSNYGG----KIPVCPAQGGGKETLKAINTSIKNKIPCVVSGGRI 326
QY 260 ADVLAAVLNQPILLVPKVAEKQKKEFPS--KHFSWEDIVRWTKLQNTSHQHLTYVD 317

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Db 327 ADVIASLVEDEAPTSSAVKEKLVFLPRTVSRLESEETESWIKWLKEILSCSHLLTVIK 386
Qy 318 FEQEGSEELDTVILKALVKACKSHSQBPQDYLDELKAVANDRVDAKSEIFNGDVEWKS 377
Db 387 MEEAGDEIVSNAISYALYKAFSTSEQDKNWNGQKLLLEWNLQDLANDEIFTNDRWES 446
Qy 378 CDLEBVMVDALVSNKPEFVRLFDVNGADVDFLTGRLOELYSRSKSLFLDLQ---R 434
Db 447 ADLQEVMTALIKDRPKFVRLFLENGNLKRLKFLTHDVLTELF-SNHFTLVYRNLIQAKN 505
Qy 435 KOEAEARLTLAGLGTQOAREPPAGPAPFSLHVEVSRLVKDFLOACRGFYQDGRPG-DRRRA 493
Db 506 SYNDALLTF-----VWKLVANFR-----RGFRKEDRNGRDEMID 539
Qy 494 EKGPAKRTGQKWLIDLNQKSENPRDLFLWAVLONRHEMATYFWAMQEGVAAALACK 553
Db 540 E-----LHDVSPITRHPLOALFIWAILQNKKLSKVITWEQTRGCTLAALGASK 587
Qy 554 ILKEMSHLETEAARATREA--KYERLALDLFSECYSNSEARAFALLVRNRNCWKTTC 611
Db 588 LKTLAKVNDINAAGESEELANEYETRAVELFTECYSDDEDLAQLLVYSCAAGGSGNC 647
Qy 612 LHLATEADAKAFFAHDGVOAFLTRIWMGDMAGTPIRLGLAFLCPALVYTNLITFSEBA 671
Db 648 LELAVEATDQHFTAQPGVQNFSLKQWYGEISRDTKNWKIILCLFIIPLVGCGFVSFRKK- 706
Qy 672 PLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQGRGPRAVELLTWRKFWGAP 731
Db 707 -----PVDKHKK-----LLWYVAFFTSP 725
Qy 732 VTVFLGNVMYFAELFTYVLLVDFRPPPGQSPGPEVTLVFWVFTLVLEIRQGFFTDE 791
Db 726 FVFSWNVVYFAELFLFAVLLMDHFHSPH---PPELVLYSLVFLVFCDEVRQVYNGV 782
Qy 792 DTHLVKFTLYYQDNWKNKCDMVAIFLIVGVTCRM---LPSAFEAGRTVLAMDFVFTLR 848
Db 783 N-----YFTDLNWNMDTLGLFFIAGIIVRLHSSNKSLSYSGRVIFCLDIYFTLR 833
Qy 849 LHIHFAHKQKGIIVERMKNQVFFLFFLSVMLVAYGVTTQALLHPHGORLEWIFRR 908
Db 834 LIHIFTVSNLGPKIIMLQRLMDIVFFFLFAVMMVAFVARQGITLRQNEQRWRIERS 893
Qy 909 VLYRVLQIPGOIPDEIDEAR---VNCS-----THPLLE-DSPSCPSLYANMLVILIL 959
Db 894 VIEPYLAMPQVPSD-VDGTVDFAHCTFTGNEKPLCVLDELHMLPR-FFENITPLV 951
Qy 960 VTFLVTVNLLMILLIAMPSTYFQVVGQADMFQRYNLIYEXHERPALAPPFILLSH 1019
Db 952 CIYMLSTNILLNLLVAMFGYTVGTQENNDQWKFQRYFLVQYCSRLNIPFPFIVFAY 1011
Qy 1020 LSLTLRRVPKKEAHKREHLERDLDPDLOQKVVTWETOKENFLSKMEKRRRDSGEVL 1079
Db 1012 FYMWVKKCFKCCCKEKNMSESSVCCPNEDNETLANEGVMKENYLVKINTKANDT-SEENR 1070
Qy 1080 KTAHRVDFTAKYLG-LREQEKIK 1103
Db 1071 HRFRQDLTKLNDLGLLKSIANKIK 1095

RESULT 11
US-09-651-236-778
; Sequence 778, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651.236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 778
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-651-236-778

Query Match 25.7%; Score 1566.5; DB 4; Length 1095;
Best Local Similarity 34.3%; Pred. No. 3.9e-144;
Matches 379; Conservative 202; Mismatches 393; Indels 131; Gaps 27;

Qy 26 GEVNFSGGKRGKRVPSGVAPSVLPDLLAEWHLPAPNLVSVLGSVEEOPPFAMKSWLR 85
Db 95 GDIQFETLGGK-GKVIRLSCDTDAEILVELLTQHHLKTPNLVSVTGGAKNFALKPRMR 153
Qy 86 DVLAKGLVKAQSTGAMILTSALRVLARHVGQAVRHSLASTSTKVRVAVGASLGRV 145
Db 154 KIFSR-LIYIAQSKGAWILTGTHYGLTKYGEVVRDNTI-SRSEENIVAIGIAWGMV 211
Qy 146 LHRRLTLE---EAQEDFPVHYPEDDGGSGQGLCSLSDLSNLSHFLVPEPPGKDGLTLELR 202
Db 212 SNRDTLRNCDAEGYFLAQYLMDD-FTRDPLYILDNHHTHLLVDVNGCHGHTPTVEAKLRN 270
Qy 203 RLEKHISB---ORAGYGGTGSIEIPVCLLVNGDPNTLERISRAVEAAPMLILVSGGI 259
Db 271 QLEKHISERTQDSNYG---KIPVCAQGGKGTALKAINTSIKNKIPCVVVEGSGRI 326
Qy 260 ADVLAALVNPQHLVVKVAEKQFKEKFPSS-KHFSWEDIIVRTWKLQNTSHOHLITVYD 317
Db 327 ADVIASLVEDEAPTSSAVKEKLVFLPRTVSRLESEETESWIKWLKEILSCSHLLTVIK 386
Qy 318 FEQEGSEELDTVILKALVKACKSHSQBPQDYLDELKAVANDRVDAKSEIFNGDVEWKS 377
Db 387 MEEAGDEIVSNAISYALYKAFSTSEQDKNWNGQKLLLEWNLQDLANDEIFTNDRWES 446
Qy 378 CDLEBVMVDALVSNKPEFVRLFDVNGADVDFLTGRLOELYSRSKSLFLDLQ---R 434
Db 447 ADLQEVMTALIKDRPKFVRLFLENGNLKRLKFLTHDVLTELF-SNHFTLVYRNLIQAKN 505
Qy 435 KOEAEARLTLAGLGTQOAREPPAGPAPFSLHVEVSRLVKDFLOACRGFYQDGRPG-DRRRA 493
Db 506 SYNDALLTF-----VWKLVANFR-----RGFRKEDRNGRDEMID 539
Qy 494 EKGPAKRTGQKWLIDLNQKSENPRDLFLWAVLONRHEMATYFWAMQEGVAAALACK 553
Db 540 E-----LHDVSPITRHPLOALFIWAILQNKKLSKVITWEQTRGCTLAALGASK 587
Qy 554 ILKEMSHLETEAARATREA--KYERLALDLFSECYSNSEARAFALLVRNRNCWKTTC 611
Db 588 LKTLAKVNDINAAGESEELANEYETRAVELFTECYSDDEDLAQLLVYSCAAGGSGNC 647
Qy 612 LHLATEADAKAFFAHDGVOAFLTRIWMGDMAGTPIRLGLAFLCPALVYTNLITFSEBA 671
Db 648 LELAVEATDQHFTAQPGVQNFSLKQWYGEISRDTKNWKIILCLFIIPLVGCGFVSFRKK- 706
Qy 672 PLRTGLEDLQDLSDLTEKSPLYGLQSRVEELVEAPRAQGRGPRAVELLTWRKFWGAP 731
Db 707 -----PVDKHKK-----LLWYVAFFTSP 725

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QY 732 VTFLGNVMPFAELFTYVLLVDPRPPQSGPPEVTLYFWVFTLVLEIRQGFTE 791
Db 726 FVFSMNWVFIATLLFAYVLLMDPHSVPH---PPELVLSLVFVLCDEVRQWVNGV 782
QY 792 DTHLVKKFTLVGDNWKNKDMVAIFLPIVGTCTRM---LPSAFAGRTVLAMDFWVFTLR 848
Db 783 N-----YFTDLNVMVMDTLGLFYFIAGIVFRLHSSKSSLYSGRVIFCLDYIIFTLR 833
QY 849 LIHIFAIHKOLGPKIIVVERMKDVFFFLFSLVWLVAYGVTTOALLHPHDCRLSWIFRR 908
Db 834 LIHIFTVSRNLGPKIIMLQRMGLIDVFFFLFAVMVAVFVARQGLRQNEQRWIFRS 893
QY 909 VLYRPIYQIFGOPLDDEAR---VNCS-----THPLLE-DSPSCPSLVANWLVILL 959
Db 894 VIYEPYLAHQVPSD-VDGTTYDFAHCTFTGNEKFLCVELDEHNLPR-FPEWITPLV 951
QY 960 VTFLVTVNLLMILLAMFSYFQVQGNADMFVKFQRYNLIYEHYERPALAPPFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTVOENNDQWKFQRYFLVQVYCSRLNIPFPFIVFAY 1011
QY 1020 LSLTLRVFKKEAHEKREHLERDLPDLPDQKVVTWETVOKENFLSKMEKRRRSEGEVLR 1079
Db 1012 FYMVVKKCFKCCCKEKNWESSVCCPKNEDNETLAWGVKENVLYVNTKANDT-SEEMR 1070
QY 1080 KTAHRVDFIAKYLGG-LRQEKRIK 1103
Db 1071 HRFRQDVTKLDLKGLLAEIANKIK 1095

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RESULT 12

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US-09-636-215-780
; Sequence 780, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(1095)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-636-215-780

```

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Query Match 25.6%; Score 1558.5; DB 4; Length 1095;
Best Local Similarity 34.1%; Pred. No. 2.4e-143;
Matches 377; Conservative 203; Mismatches 394; Indels 131; Gaps 27;
QY 26 GEVNFSGSKKRGKFRVPSGVAPSLFDLLAEHLPAENLVLSVCEQPFAMKSWLR 85

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Db 95 GDIOFETLGGK-GKIRISCDTDAIBILYELLTQHWHLKTNLNLVSVTGGAKNFALKPRMR 153
QY 86 DVLKGLVKAAGSTGAWILTALRVGLARHVGQAVROHSLASTSTKRVVAVGASIGRV 145
Db 154 KIFSR-LIYIAOSKAGWILTGTGYGLMKYIGEVVRDNTI-SRSSEENIYVIGIAAGMV 211
QY 146 LHRRIIE---EAQEDFPVHYPEDGGGQPLCSLDSNLSHFILLVEFPFGPKGDLTELR 202
Db 212 SNRDTLIRNCABGYFLAQLMDD-FTRDPLYLIDNNHTLLLDVNGCHGHPVTEAKLN 270
QY 203 RLEKHISE---ORAGYGTGSIIEIPVLCILVNGDPNLTBRISRAVQAAPMILLVSGGI 259
Db 271 QLEKIYISERTIQDSNYGG---KIPVCPAQQGKETLKAINTSIKNTKPCVVVVGSGOI 326
QY 260 ADVLAALVNPHLLVPAKQKPKKPPS---KHFSWEDIVRWTKLLQNTSHQHLITVVD 317
Db 327 ADVIASLVEVEDALTSSAVKEKLVRFPLRTVSRLEPEETESIKWLKEILECSHLLTVIK 386
QY 318 FEQSGSELDVTILKLVACKSHSQEPQDYLDELKLAAMDVDIAKSEIFNGVVEWKS 377
Db 387 MEZAGDSIVSNALSYALYKAFSTSEQDKDNWNGQLKLLLEWNLQDLANDEIFTNDRWES 446
QY 378 CDLEEVMVDALVSNKPEFVRLFVDNCAVDPLTYGRLOELYSVSRKSLFDLLQ---R 434
Db 447 ADLQEVMTALIKDRPKFVRLFENGLMLRKLTHDVLTELF-SNHFTSLVYRNLIQAKN 505
QY 435 KQEEARLTLAGTQOAREPPAGPPAFSLHEVSRVLKDFLQDACRGFFVODRPG-DRRA 493
Db 506 SYNDALLTF-----VMLVANFR-----RGFRKDRDRGRDMDI 539
QY 494 EKGPAKRPTGQKWLDDLKQSENPMRDLFLWAVLONRHEMATYPMWQBGVAAAALAA 553
Db 540 E-----LHDVSPITRHPQLQALFIALLONKELSKVITWETRGTCTLLAALGASK 587
QY 554 ILKEMSHLETEARARATREA---KYERLALDLFSECYSNSEARAFALLVRNRCWKTTC 611
Db 588 LLKTLAKVKNIDINAAESEBELANEYETRAVELTECVSSDEDLAEQLLYSCAMGSGNC 647
QY 612 LHLATEADAKAFFAHDGVQAFTRIWMGMAACTPILRLGAPLCPALVYTNLIITFSEA 671
Db 648 LELAVEATDQHFIAQPGVQNFSLQWYGEISRTQWKIILCLFIPLVCGCFVSRKK- 706
QY 672 PLRTGLELDQLDLSLDEKSPLYGLOSERVEELVEAPRAQGRGPRAVFLLTWRKFWGAP 731
Db 707 -----FVDKHKK-----LLWYVAFPTSP 725
QY 732 VTFLGNVMPFAELFTYVLLVDPRPPQSGPPEVTLYFWVFTLVLEIRQGFTE 791
Db 726 FVFSMNWVFIATLLFAYVLLMDPHSVPH---PPELVLSLVFVLCDEVRQWVNGV 782
QY 792 DTHLVKKFTLVGDNWKNKDMVAIFLPIVGTCTRM---LPSAFAGRTVLAMDFWVFTLR 848
Db 783 N-----YFTDLNVMVMDTLGLFYFIAGIVFRLHSSKSSLYSGRVIFCLDYIIFTLR 833
QY 849 LIHIFAIHKOLGPKIIVVERMKDVFFFLFSLVWLVAYGVTTOALLHPHDCRLSWIFRR 908
Db 834 LIHIFTVSRNLGPKIIMLQRMGLIDVFFFLFAVMVAVFVARQGLRQNEQRWIFRS 893
QY 909 VLYRPIYQIFGOPLDDEAR---VNCS-----THPLLE-DSPSCPSLVANWLVILL 959
Db 894 VIYEPYLAHQVPSD-VDGTTYDFAHCTFTGNEKFLCVELDEHNLPR-FPEWITPLV 951
QY 960 VTFLVTVNLLMILLAMFSYFQVQGNADMFVKFQRYNLIYEHYERPALAPPFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTVOENNDQWKFQRYFLVQVYCSRLNIPFPFIVFAY 1011
QY 1020 LSLTLRVFKKEAHEKREHLERDLPDLPDQKVVTWETVOKENFLSKMEKRRRSEGEVLR 1079
Db 1012 FYMVVKKCFKCCCKEKNWESSVCCPKNEDNETLAWGVKENVLYVNTKANDT-SEEMR 1070
QY 1080 KTAHRVDFIAKYLGG-LRQEKRIK 1103

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Db	1071	HRFQDTPKLNLDKGLLKEIANKIK	1095
RESULT 13			
US-09-685-166A-780			
; Sequence 780, Application US/09685166A			
; Patent No. 6630305			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yuqi			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Day, Craig H.			
; APPLICANT: Vedwick, Thomas S.			
; APPLICANT: Carter, Darrick			
; APPLICANT: Li, Samuel			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A.W.			
; APPLICANT: Hepler, William			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; FILE REFERENCE: 210121.427C21			
; CURRENT APPLICATION NUMBER: US/09/685,166A			
; CURRENT FILING DATE: 2000-10-10			
; NUMBER OF SEQ ID NOS: 898			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 780			
; LENGTH: 1095			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: VARIANT			
; LOCATION: (1)...(1095)			
; OTHER INFORMATION: Xaa = Any Amino Acid			
US-09-685-166A-780			
Query Match 25.6%; Score 1558.5; DB 4; Length 1095;			
Best Local Similarity 34.1%; Pred. No. 2.4e-143; Indels 131; Gaps 27;			
Matches 377; Conservative 203; Mismatches 394;			
Qy	26	GEVNFPGGKRGKGFVRVPSGVAPSVLFDLLAEHLAPNLVSLVSGEEQPFAMKSMRLR	85
Db	95	GDIQFETLGGK-GKIRLSCDTPDAEILYELLTQHWHLKTPLNVLISVTGGAKNFALKPRMR	153
Qy	86	DVLRKGLVKAAOSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMASLGRV	145
Db	154	KIFSR-LIVIAOSKGAWILTGTHYGLMKYIGEVVRDNTI-SRSSEENIVAIIGIAWGMV	211
Qy	146	LHRRILE---EAQEDPPVHPDDGSGQGLCSLSDNLSHFLVILVERPPGKDGTLRL	202
Db	212	SNRDTLIRNCDAEGYFLAQLMDD-FTRDPLYILDNNHTLLLVONGCHGHTVEAKLRN	270
Qy	203	RLKHLISE---ORAGYGGTGSIEIPVLCLLVNGDPNTRERISRAVEQAAPWILVSGGI	259
Db	271	QLEKYSERTIQDSNYGG---KIPVCAQGGKGTAKINTSIKNKIPCVVVEGGQI	326
Qy	260	ADVLAALVNQPHLLVPKVAEKQPEKFPSS--KHFSWEDIVRWTKLLQNTISHQLLTVDYD	317
Db	327	ADVIASLVEVEDALTSVAKEKLVRLPRTVSRLPPEETESWIKLKEILECSHLLTVTK	386
Qy	318	FEQEGSEELDTVLKALVKACKSHSQEPQDYLDELKLAVDNRDVTAKSEIENGDVIEWS	377
Db	387	MEAGDEIVSNATSYALYAFSTSEQDKONWNGQLKLLLEWQDLNDEIFNDRRWS	446
Qy	378	CDLEEVVADALVSNKPEFVRLFDVNGADVADFLTYGRLOELVRSVRKSKLLFDLQ---R	434
Db	447	ADLQEVNFTALIKDRPKFVRLFLENGLNLRKFLTHVDVITELF-SNHFSTLVYRNLIQAKN	505
Qy	435	KOBEARLTLAGLGTQOQAREPPAGPPAPFASLHEVSRVLKDFLODACRGYQDGRPG-DRRRA	493
Db	506	SYNDALLTF-----VWKLVANFR---RGPRKEDRNGRDEMDI	539
Qy	494	EKGPAPKPTCQKWLNDLNQKSENPRDLFLWAVLQNRHEMATYFWANGQSGVAALAAACK	553
Db	540	E-----LHDVSPITRHPLOALFIWALQNKKEISKVITWQTRGCTLAUGASK	587
Qy	554	ILKEMSHLETEAARATREA--KYERLALDLFSECYSNSEARAFALLVRRNRCSKTTTC	611
Db	588	LLKTLAKVKNDINRAGESEBELANEYETRAVELTECYSSDEDLAEQLLVVSCAAGSNC	647
Qy	612	LHLATEADAKAFFAHGCVQAPLTRIWMGDMAAGPPIRLRLGAFICPALVYTNLTFSSEA	671
Db	648	LELAVENTDQHFIAPQGVQNFSLSKWYGEISRDTKNWKILCLFIILVPGCGFVSFRKK-	706
Qy	672	PLRTGLEDLQDLSLDEKSPFLYGLQSRVEELVEAPRAQDGRGPRAVFLTRRKKFWCAP	731
Db	707	-----PVDKHK-----LMWYVAFFTSP	725
Qy	732	VTVFLGNVMYFAFLFTVLLVDRPPPOGPGSPGVTLVFWVFTLVLEIRQGFETDE	791
Db	726	FVFSWNVVFIALLFAYVLLMDFHSPH---PPELVLYSLVFLVFCDEVQWYNGV	782
Qy	792	DTHLVKFKFTLYVGNWNKCDMAVIFLFIIVGVTCRM---LPSAFBAGRTVLAMDPMVFTLR	848
Db	783	N-----YFTDLWNVMDTGLFYFIAGIVFRLHSSNKSLSYSGRVIFCLDIIFTLR	833
Qy	849	LIHIPAIHKQIGPKIIVVERMKDVFFFLPFLSVLVAYGVTTQALLPHDGRLEWIERR	908
Db	834	LIHIFTVSRNLGPKIIMLQRLIDVFFFLFAXMVAFGVARQOILQRNQRWRWIFRS	893
Qy	909	VLXRPYLOIGQIPLDEIDEAR---VNCS-----THPLLE-DSPSCPSLVANMLVILL	959
Db	894	VIYEPYLAHQGVPSD-VDGTYYDFAHCTFTGNESKPLCVLDELHNLR-PFENITPLV	951
Qy	960	VTFLVTVNVLNLLIAMFSYTFVQGNADMFWKFORNYLIVEYHERPALAPPFILLSH	1019
Db	952	CIYMLSTNILLVNLVAMFGYTVGVQNNQWVKFQRYFLVQVYCSRLNIPFPFIVPAY	1011
Qy	1020	LSLTLRVFKKEABHKREHLERDLPDLDQKVVTWETVKENFLSKMEKRDRDSEGLR	1079
Db	1012	FYMWVKCFKCKCKCKNMESSVCCFKNEDNETLAWEGVMKENYLVKINTKANDT-SEEMR	1070
Qy	1080	KTAHRVDYFIKVLGG-LRQEKRIK	1103
Db	1071	HRFQDTPKLNLDKGLLKEIANKIK	1095
RESULT 14			
US-09-679-426-780			
; Sequence 780, Application US/09679426			
; Patent No. 6759515			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; APPLICANT: Dillon, Davin C.			
; APPLICANT: Mitcham, Jennifer L.			
; APPLICANT: Harlocker, Susan L.			
; APPLICANT: Jiang, Yuqi			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Retter, Marc W.			
; APPLICANT: Stolk, John A.			
; APPLICANT: Vedwick, Thomas S.			
; APPLICANT: Carter, Darrick			
; APPLICANT: Li, Samuel			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A.W.			
; APPLICANT: Hepler, William			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			

```

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1095)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-679-426-780

Query Match
Best Local Similarity 25.6%; Score 1558.5; DB 4; Length 1095;
Matches 377; Conservative 203; Mismatches 394; Indels 131; Gaps 27;

26 GEVNFSGGSKKGFVVPVSGVAPSVLFDLLLAELWHLPAAPNLVSLVSGEQQPAMKSWLR 85
95 GDIQFETLGKK-GKYIRLSCTDABEILYELLTQHHLKTNLVISVSGGAKFALPRMR 153
86 DVLKRGKLVKAAQSTGAWILTALVGLARHVQAVRDHSLASTSTKRVVAVGMSLGRV 145
154 KIFSR-LYIAQSGKAWILTGGTHYGLMKYIGEVRDNTI-SRSSENIVAIGIAAGMV 211
146 LHRRLT---EAQEDFPVHYEDDGGGQGLCSLDSNLSHFILVSPGPKGDLTELR 202
212 SNRDTLRNCAEGVFLAQLMDD-FTRDPLYLDNNHTLLVLDGCHGHPVTEAKLSN 270
203 RLEKHIS--ORAGYGGTSGIETPVLCLLVNGDPTLERISRAVQAAAPMLITVSGGI 259
271 QLEKYISERTQDSNYGG---KIPVCFAGGGGKELKAINTSIKNKIPCVVVEGSGI 326
260 ADVLAALVNPHLLVPPKVAEKQKPPS--KHFSWEDIVRTKLLONTSHQHLITVVD 317
327 ADVIASLVEVEDALTSAVKEKLVFLPRVSRLPPEETESIKMLKEILECSHLLTVIK 386
318 FEQSGSELTOTVILKALVACKSHSQEPDYDELKLAVAMDRVDIAKSEIFPNGVEMKS 377
387 MEAGDEIVSNALSYALYAFSTSEQDKNNWQGLKLEWNLQDLANDLFTNDRWES 446
378 CDLEEVMDALVNKPEFVRLFDVNGADVADFLTVGRLOELYSVSRKSLFLDLQ---R 434
447 ADLQEVMTALIKDRPKFVRLFENGLNRKFLTHDVITELF-SNHFSTLVYRNLQIAKN 505
435 KQEARLTLAGLTQQAEPAPGPPAFSLHESVRLKDFLODACRGFFYQDGRPG-DRRRA 493
506 SYNDALTF-----VWKLVANFR---RGFRKEDNRGDEMDI 539
494 EKGPAKRP7GQKWLDDNOKSNPNWRDLFLNAVLONRHEMATYFWAMQGEVAAALACK 553
540 E-----LHDVSPITPHLOALFTWAILQNKELSVIWEQTRGCTLAALGASK 587
554 ILKEMSHLETEAARATREA--KYERLALDFSECYSNSRPAFALLVRNRCKSWTTC 611
588 LUKTLAKVGNINAAAGESEELANEYETAVELFTCYSSDEDLAEQLLVYSCAWGGSNC 647
612 LHLATEADAKFAFFHDGVQAFITRWGMDMAAGTPIRLLAGLPCALPVYTNLITFSEA 671
648 LELAVEATDQFLAQPGVQNFSLKQWYGEISRDKNWKIILCLFIPLVGCYFVSPRKK- 706
672 PLRTGLELDQLDSDTEKSPLYGLQSRVBELVEAPRAQGRDPRFVALLTRWRKFWGAP 731
707 -----FVDKHKK-----LLWYVAFFTSP 725
732 VTVEFGNVVMYFALEFLFTVYLLVVDPRPPQSGSGEVTLYFWFTLVLEEIRQGFTDE 791
726 FVFSMNWVFIAPLLFAVLLMDFHSVPH---PPELVLSLVFVFLFCDEVRQWYNGV 782
792 DTHLVKFTLYVGDNNWKNCDMVAIFLIVGVTCRM---LPSAFEAGRTVLANDFVFTLR 848

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Db 154 KIFSR-LIYIAQSGAWILTGTHYGLMKYIGEVVRDNTI-SRSSEENIVAIGIAAMGMV 211
Qy 146 LHRRILE---EAQEDFPVHYEDDCGSOPLCSLDSNLSHPLIYEPGPGKGDGLTELRL 202
Db 212 SNRDTLIRNCDAEGYFLAQYLMDD-FTRDPLYILDNNHTHLLVDNGCHGHTTVEAKURN 270
Qy 203 RLEKHISE---ORAGYGGTGSIEIPVGLLVNGDPNTLIERISRAVEQAAPMLILVSGSGI 259
Db 271 QLEKIYISERTIQDSNYG---KIPVCAQGGGKETLKAINTSIKNKIPCVVVEGSGOI 326
Qy 260 ADVLAALVNQPHLLVPKVAQKFKKPPS--KHFSWEDIVRWTKLLQNLITSHQHLLTYVD 317
Db 327 ADVIASLVEVEDALTSSAWEKELRFLPRTVSRLPPEETESMIKWLKEILECSHLLTVIK 386
Qy 318 FQEGSEBELDTVILKALVKACKSHSQEPQDYLDELKJAVANDRVDIKSEIFNGDVENKS 377
Db 387 MEEAGDEIVSNAISVALYKAFSTSQDKDNWNGQLKLLLEMNQDLANDEIFTNDRWES 446
Qy 378 CDEEVMVDALVSNKPEFVRLFVDNGADVADVFITYGRLOELYRSVSRSKSLFLDLLQ---R 434
Db 447 ADLQEVMTALIKDRPKFVRLFLEGNLNRKFLTHDVLTELP-SNHFSTLVYRNLIQAKN 505
Qy 435 KOEEARLITLAGLGTQOAREPPAGPPAFSLHVSRLVKDFLODACRGFYODGRPG-DRRRA 493
Db 506 SYNDALLTF-----VWKLVANPR---RGFRKEDRNGRDEMID 539
Qy 494 EKGPAKPTGQKWLIDLNLKSENPRDPLFMAVLQNRHEMATYFWAMQOEGVAAALAAACK 553
Db 540 E-----LHDVSPITRHPLOALFIAWILQNKLSKVIWEQTRGCTLAALGASK 587
Qy 554 ILKEMSHLEAEAAABATREA--KYERLALDLFSECYSNSEARAFALLVRRNRKWSKTTTC 611
Db 588 LKTLAKVNDINAAGESEELANEYETRAVELFTECISDEDLAEQLLVYSCAMGGSNC 647
Qy 612 LHLATEADAKAPFAHDGVAFLTRIWMGDMAAGTPIRLILGALPCALPVYTNLITPSEEA 671
Db 648 LELAPEATQHFIAQFGVQNFLSQWYGEISRDTKWKIILCLFIPLVCGCGVSRKK- 706
Qy 672 PLRTGLELDLQSLDTEKSPLYGLQSRVEELVEAPRAQDRGPRAVFLITRWKFWGAP 731
Db 707 -----PVDKHKK-----LLWYVVAFFTSPT 725
Qy 732 VTVELGNVMYFAFLFTVYLLVDFRPPPPQSPGPEVTLYFWVFTLVLEEIRQGFETDE 791
Db 726 FVVFSSNVVFIYAFLLLFAYLLVLMDFHSVPH---PEELVLYSLVFLFCDEVROQWYNGV 782
Qy 792 DTHLVKFTLYVGDNNKCDMVAIFLFIIVGVTCRM---LPSAFEAGRTVLAMDVMVFTLR 848
Db 783 N-----YFTDLNVMVDTLGLFYFIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLR 833
Qy 849 LIHIFAIHKQLGPKIIVVERMMKDVFFLFFLSVWLVAYGVTTOALLHPHDGRLIEWIFRR 908
Db 834 LIHIFTVSRNLGPKIIMLQRLMIDVFFFLFAXMMVAFGARQGLRQNEQRWRWIFRS 893
Qy 909 VLYRPLVQIFGOJPLDEIDEAR---VNCS-----THPLILLE-DSPSCPSLYANMLVILL 959
Db 894 VIYEPYLFAMFGQVPSD-VDGTTFVDFACTPTGNEKSPCLCVELDEHNLPR-FPEWITIPLV 951
Qy 960 VTFLLVNVLMLLMTAMFSYTFQVQGNADMFWKFORYNLIYVEYHERPALAPFFILLSH 1019
Db 952 CIYMLSTNILLVNLVAMFGYTVGTQENNDQVWKQRYFLVQBYCSRLNIPFFIVFAY 1011
Qy 1020 LSLTLRVPFKAEABHREHLERDLDPDLQKVVTWETVQENFLSKMEKRRRSEGEVLR 1079
Db 1012 FYWVVKCFKCCCKEKNMSSVCCFKNEDNETLAWEGWMKENYLVKINTKANDT-SEEMR 1070
Qy 1080 KTAHRVDVFIKYLGG-LRQEKRIK 1103
Db 1071 HRFRLQDLKLDLKLKEIANKIK 1095

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 18:19:05 ; Search time 175 Seconds
(without alignments)
2556.207 Million cell updates/sec

Title: US-09-834-792D-4
Perfect score: 6093
Sequence: 1 MQDVQPRPGSGDAEDRRE.....HRGGLDGWEQPGAGQPPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6093	100.0	1165	13	US-10-026-188-8
2	6093	100.0	1165	16	US-10-408-765A-1150
3	6093	100.0	1165	17	US-10-785-758-2
4	6078	99.8	1167	16	US-10-794-897-2
5	6057.5	99.4	1164	9	US-09-834-792-5
6	5985	98.2	1165	16	US-10-794-897-7
7	5134.5	84.3	1168	16	US-10-794-897-8
8	5088.5	83.5	1158	9	US-09-834-792-2
9	5088.5	83.5	1158	13	US-10-026-188-5
10	5088.5	83.5	1158	16	US-10-794-897-4
11	5025.5	82.5	1156	16	US-10-794-897-6

12	5008.5	82.2	1165	13	US-10-026-188-2	Sequence 2, Appli
13	2448.5	40.2	1166	15	US-10-295-027-558	Sequence 558, App
14	2448.5	40.2	1166	15	US-10-295-027-916	Sequence 916, App
15	2448.5	40.2	1214	14	US-10-142-649-2	Sequence 2, Appli
16	2448.5	40.2	1214	17	US-10-789-378-80	Sequence 80, Appli
17	2448.5	40.2	1214	17	US-10-847-918-30	Sequence 30, Appli
18	2448.5	40.1	1214	15	US-10-343-114-10	Sequence 10, Appli
19	2428	39.8	1127	16	US-10-643-795A-123	Sequence 123, App
20	2428	39.8	1127	17	US-10-948-518-123	Sequence 123, App
21	2412.5	39.6	1129	15	US-10-391-399-2	Sequence 2, Appli
22	2353	38.6	1083	9	US-09-789-481C-2	Sequence 44, Appli
23	2184.5	35.9	1040	16	US-10-312-354-44	Sequence 1, Appli
24	2039	33.5	1503	13	US-10-007-706-1	Sequence 104, App
25	2039	33.5	1503	14	US-10-153-244-104	Sequence 21, Appl
26	2039	33.5	1503	14	US-10-210-152-21	Sequence 48, Appl
27	2039	33.5	1503	15	US-10-369-022-48	Sequence 21, Appl
28	2039	33.5	1503	15	US-10-405-793-21	Sequence 3, Appli
29	2039	33.5	1503	16	US-10-467-163-3	Sequence 54, Appl
30	2039	33.5	1503	16	US-10-757-262-54	Sequence 2, Appli
31	2039	33.5	1503	16	US-10-492-477-2	Sequence 14, Appl
32	2023.5	33.2	1507	16	US-10-492-477-14	Sequence 4, Appli
33	2011	33.0	1508	16	US-10-492-477-4	Sequence 8, Appli
34	1619	26.6	678	15	US-10-343-114-8	Sequence 8, Appli
35	1582	26.0	1104	14	US-10-171-319-8	Sequence 1, Appli
36	1567.5	25.7	1104	15	US-10-352-724-1	Sequence 778, App
37	1566.5	25.7	1095	9	US-09-759-143-778	Sequence 778, App
38	1566.5	25.7	1095	9	US-09-780-669-778	Sequence 778, App
39	1566.5	25.7	1095	9	US-09-822-827-778	Sequence 778, App
40	1566.5	25.7	1095	9	US-09-895-793-778	Sequence 778, App
41	1566.5	25.7	1095	9	US-09-895-814-778	Sequence 778, App
42	1566.5	25.7	1095	13	US-10-012-896-778	Sequence 421, App
43	1566.5	25.7	1095	14	US-10-205-823-421	Sequence 778, App
44	1566.5	25.7	1095	14	US-10-144-678A-778	Sequence 778, App
45	1566.5	25.7	1095	14	US-10-294-025-778	Sequence 778, App

ALIGNMENTS

RESULT 1
US-10-026-188-8
Sequence 8, Application US/10026188
Publication No. US20020164645A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Zhang, Yifeng
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
FILE REFERENCE: 02307E-114910US
CURRENT APPLICATION NUMBER: US/10/026,188
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/259,379
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 1165
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human ltrpc6
US-10-026-188-8

Query Match	100.0%;	Score	6093;	DB	13;	Length	1165;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	1165;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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DB	1	MQDVQPRPGSGDAEDRRELGLHGEVNFVGGSKKGFVRVPSGVAPSVLFDLLAEW	60				
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Db 61 HLPAPNLVSLVGEQGFAMKSWLRDLVLRGLVKAQSTGAWILTSALRVGLARHVQAV 120
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QY 301 KLLQNTITSHQHLTVYDFEQSGSEELDTVLKALVKAQSHSQEPQDYLDELKLA VAWDR 360
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QY 361 VDIKSEIFNGDVWKSQDLEEMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOEL YR 420
Db 361 VDIKSEIFNGDVWKSQDLEEMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOEL YR 420
QY 421 SVSRKSLFFDLQKQEBEARLTLAGLGTQQAEPFAPFSLHEVSRVLKDFLQDACRG 480
Db 421 SVSRKSLFFDLQKQEBEARLTLAGLGTQQAEPFAPFSLHEVSRVLKDFLQDACRG 480
QY 481 FYQDGRPGDRAEKGPAKPTGQKWLDDLNOKSENPRDLFLMAVLQNRHEMATYFWAM 540
Db 481 FYQDGRPGDRAEKGPAKPTGQKWLDDLNOKSENPRDLFLMAVLQNRHEMATYFWAM 540
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Db 541 GQGVAAALAAACKILKEMSHLETEAARAATREAKYERLALDLFSECYNSSEARAFALLV 600
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QY 661 YTNLITFSEEAFLRTGLDQLDSDTEKSPLYGLQSRVEELVEAPRAQDGRPAVFL 720
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QY 901 RLEWIFRVLRYPIQIFGQPLDEIDEARVNCSTHPLLEDSPCSLYANWLIVLLV 960
Db 901 RLEWIFRVLRYPIQIFGQPLDEIDEARVNCSTHPLLEDSPCSLYANWLIVLLV 960
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QY 1081 TAHRVDFIAKYLGLREQEKIKCLESQINCSVLVSSVADVLQGGGPRSSQCHGGSQ 1140
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Db 1141 LVAADHRGGLDQWQPGAGQPPSDT 1165
RESULT 2
US-10-408-765A-1150
; Sequence 1150, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1150
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1150
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 HLPAPNLVSLVGEQGFAMKSWLRDLVLRGLVKAQSTGAWILTSALRVGLARHVQAV 120
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QY 181 SHFILVEPPGKDGTLRLRLKHLSEQRAGYGGTGSIEIPVLCLLVNGDPNTLRI 240
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QY 241 SRAVEQAAPWLLVSGGGIADVLAAVNOPHLLVPKVAEKQPKFPPSKHFSWEDIVRWT 300
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Qy	721	LTRWRKFWGAPVTVFLGNVVMYFAFLFTVLLVDFRPPQPGSGPEVTLYFWVFTLV	780
Db	721	LTRWRKFWGAPVTVFLGNVVMYFAFLFTVLLVDFRPPQPGSGPEVTLYFWVFTLV	780
Qy	781	BEIRQGFPTDTHLVKFKFTLYVGDNNKCDMVAIFLFIIVGVTICRMLPSAFEAGRTVLAM	840
Db	781	BEIRQGFPTDTHLVKFKFTLYVGDNNKCDMVAIFLFIIVGVTICRMLPSAFEAGRTVLAM	840
Qy	841	DFWVFTLRLIHI FAIHKQLGPKII VVERMKDKVFFFLFSVWLVAVGVTTQALLHPHDG	900
Db	841	DFWVFTLRLIHI FAIHKQLGPKII VVERMKDKVFFFLFSVWLVAVGVTTQALLHPHDG	900
Qy	901	RLEWIFRVLRYRPIQIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLIVILLV	960
Db	901	RLEWIFRVLRYRPIQIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLIVILLV	960
Qy	961	TFLVNTVLLMNLIIAMFSYTFQVVGNDMFWKFORYNLIVEYHERPALAPPFILLSHL	1020
Db	961	TFLVNTVLLMNLIIAMFSYTFQVVGNDMFWKFORYNLIVEYHERPALAPPFILLSHL	1020
Qy	1021	SILTRARVFKGAEHREHLERDLPDLPDQKVVTWETVQENFLSKWEKRRRDSGEVLURK	1080
Db	1021	SILTRARVFKGAEHREHLERDLPDLPDQKVVTWETVQENFLSKWEKRRRDSGEVLURK	1080
Qy	1081	TAHRVDFITAKYLGGLRGEQEKRIKCLSQINYSVLVSSVADVLAQGGGPRSSQHCGESQ	1140
Db	1081	TAHRVDFITAKYLGGLRGEQEKRIKCLSQINYSVLVSSVADVLAQGGGPRSSQHCGESQ	1140
Qy	1141	LVAADHRGGLDGEQPGAGQPPSDT	1165
Db	1141	LVAADHRGGLDGEQPGAGQPPSDT	1165

RESULT 3

US-10-785-758-2
; Sequence 2, Application US/10785758
; Publication No. US20050019830A1
; GENERAL INFORMATION:
; APPLICANT: Penner, Reinhold
; APPLICANT: Flieg, Andrea
; TITLE OF INVENTION: Methods of Screening for TRPM5 Modulators
; FILE REFERENCE: A-72155/RET/THR (469324-00029)
; CURRENT APPLICATION NUMBER: US/10/785,758
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/448,955
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-785-758-2

Query Match 100.0%; Score 6093; DB 17; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MODVQGPGRGSDAEDRELGLHRGEVNFVGGSGKKRKFVRVPSPVAPSVLPDILLAEW	60
Qy	61	HLPAPLNVLVSGEEQPFAMKSWLRDLRLKGLVKAAQSTGAWITLSALRVGLARHVQAV	120
Db	61	HLPAPLNVLVSGEEQPFAMKSWLRDLRLKGLVKAAQSTGAWITLSALRVGLARHVQAV	120

Qy	121	RDHSLASTSTKVRVAVGMASLGRVLRHRRILEAQEDFPVHYBEDDGGSGGPLICSLDSNL	180
Db	121	RDHSLASTSTKVRVAVGMASLGRVLRHRRILEAQEDFPVHYBEDDGGSGGPLICSLDSNL	180
Qy	181	SHFILVEPGPGKDGITELRLERLKHISEQRAGYGGTSGIEIPVCLLVNGDPNTERI	240
Db	181	SHFILVEPGPGKDGITELRLERLKHISEQRAGYGGTSGIEIPVCLLVNGDPNTERI	240
Qy	241	SRAVEQAAPMLIIVGSGGIADVLAAALVNQPHLLVPKVAEKQFKEKFPFSKHSFWMEDIVRWT	300
Db	241	SRAVEQAAPMLIIVGSGGIADVLAAALVNQPHLLVPKVAEKQFKEKFPFSKHSFWMEDIVRWT	300
Qy	301	KLQNTITSHOHLITVDFPQEGSEELDTVILKALVKACKSHSQBPQDYLDLKLAVAWDR	360
Db	301	KLQNTITSHOHLITVDFPQEGSEELDTVILKALVKACKSHSQBPQDYLDLKLAVAWDR	360
Qy	361	VDIAKSEIFNGDVEWKSCLDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR	420
Db	361	VDIAKSEIFNGDVEWKSCLDEEVMVDALVSNKPEFVRLFVDNGADVADFLTYGRLOELYR	420
Qy	421	SVSRKSLFLLQRLQKQEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRLVKDFLQDACRG	480
Db	421	SVSRKSLFLLQRLQKQEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSRLVKDFLQDACRG	480
Qy	481	FYQDGRPCDRRRAEKGPAPKPTGQKWLDDNOKSENWRDLFLWAVLQNRHEMATYFWAM	540
Db	481	FYQDGRPCDRRRAEKGPAPKPTGQKWLDDNOKSENWRDLFLWAVLQNRHEMATYFWAM	540
Qy	541	GOEGVAAALAAACKTILKEMSHLETEAARATREAKYERLADLDFSECVSNEARAFALLV	600
Db	541	GOEGVAAALAAACKTILKEMSHLETEAARATREAKYERLADLDFSECVSNEARAFALLV	600
Qy	601	RRNCWSKTTCLHLATADAKAFPAHGDVQAFTRIWWGDMAAGTPIRLLLGFLCPALV	660
Db	601	RRNCWSKTTCLHLATADAKAFPAHGDVQAFTRIWWGDMAAGTPIRLLLGFLCPALV	660
Qy	661	YTNLITFSEAPLRTGLDLDLQDLSLDTKESPLVGLQSRVEELVEAPRAQDGRGPRAVFL	720
Db	661	YTNLITFSEAPLRTGLDLDLQDLSLDTKESPLVGLQSRVEELVEAPRAQDGRGPRAVFL	720
Qy	721	LTRWRKFWGAPVTVFLGNVVMYFAFLFTVLLVDFRPPQPGSGPEVTLYFWVFTLV	780
Db	721	LTRWRKFWGAPVTVFLGNVVMYFAFLFTVLLVDFRPPQPGSGPEVTLYFWVFTLV	780
Qy	781	BEIRQGFPTDTHLVKFKFTLYVGDNNKCDMVAIFLFIIVGVTICRMLPSAFEAGRTVLAM	840
Db	781	BEIRQGFPTDTHLVKFKFTLYVGDNNKCDMVAIFLFIIVGVTICRMLPSAFEAGRTVLAM	840
Qy	841	DFWVFTLRLIHI FAIHKQLGPKII VVERMKDKVFFFLFSVWLVAVGVTTQALLHPHDG	900
Db	841	DFWVFTLRLIHI FAIHKQLGPKII VVERMKDKVFFFLFSVWLVAVGVTTQALLHPHDG	900
Qy	901	RLEWIFRVLRYRPIQIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLIVILLV	960
Db	901	RLEWIFRVLRYRPIQIFGOIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLIVILLV	960
Qy	961	TFLVNTVLLMNLIIAMFSYTFQVVGNDMFWKFORYNLIVEYHERPALAPPFILLSHL	1020
Db	961	TFLVNTVLLMNLIIAMFSYTFQVVGNDMFWKFORYNLIVEYHERPALAPPFILLSHL	1020
Qy	1021	SILTRARVFKGAEHREHLERDLPDLPDQKVVTWETVQENFLSKWEKRRRDSGEVLURK	1080
Db	1021	SILTRARVFKGAEHREHLERDLPDLPDQKVVTWETVQENFLSKWEKRRRDSGEVLURK	1080
Qy	1081	TAHRVDFITAKYLGGLRGEQEKRIKCLSQINYSVLVSSVADVLAQGGGPRSSQHCGESQ	1140
Db	1081	TAHRVDFITAKYLGGLRGEQEKRIKCLSQINYSVLVSSVADVLAQGGGPRSSQHCGESQ	1140
Qy	1141	LVAADHRGGLDGEQPGAGQPPSDT	1165
Db	1141	LVAADHRGGLDGEQPGAGQPPSDT	1165

RESULT 4

US-10-794-897-2
; Sequence 2, Application US/10794897
; Publication No. US20040259160A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Zhou, Yun-Ping
; APPLICANT: Metabolix, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; FILE REFERENCE: 016325-019010US
; CURRENT APPLICATION NUMBER: US/10794,897
; CURRENT FILING DATE: 2004-03-04
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/452,596
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human betaTRP (MTR1) calcium channel
US-10-794-897-2

Query Match 99.8%; Score 6078; DB 16; Length 1167;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1164; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MQDVQGPFGSGDADRELGHRGEVNFPGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
Db 1 MQDVQGPFGSGDADRELGHRGEVNFPGSGKRGKRVFVPSGVAPSVLFDLLAEW 60

QY 61 HLPAPNLVSLVGEQPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLRHVGQAV 120
Db 61 HLPAPNLVSLVGEQPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLRHVGQAV 120

QY 121 RDHSLASTTKRVVAVGMASLGRVLRHRLBEAQ--EDFPVHYPEDDGGSGGPLCSLDS 178
Db 121 RDHSLASTTKRVVAVGMASLGRVLRHRLBEAQVHEDFPVHYPEDDGGSGGPLCSLDS 180

QY 179 NLSHFLVLPFGPGKDGTLRLRLKHSIQAGYGGTSGIETPVLCLVNGDPNTLE 238
Db 181 NLSHFLVLPFGPGKDGTLRLRLKHSIQAGYGGTSGIETPVLCLVNGDPNTLE 240

QY 239 RISRAVEQAAPWLLVVGSGGIADVLAAVNPQLLVKVAEKQKFKFPKHSFWSWEDIVR 298
Db 241 RISRAVEQAAPWLLVVGSGGIADVLAAVNPQLLVKVAEKQKFKFPKHSFWSWEDIVR 300

QY 299 WTKLLQNTITSHOHLTVYDFQEGSEELDTVLKALVKACKSHSQBPQDYLDLKLAVAW 358
Db 301 WTKLLQNTITSHOHLTVYDFQEGSEELDTVLKALVKACKSHSQBPQDYLDLKLAVAW 360

QY 359 DRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOEL 418
Db 361 DRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLFDVNGADVADFLTYGRLOEL 420

QY 419 YRSVSRKSLLDLQKQSEARLTLAGLGTQQAEPAGPPAPSLHVSRLKDFLQDAC 478
Db 421 YRSVSRKSLLDLQKQSEARLTLAGLGTQQAEPAGPPAPSLHVSRLKDFLQDAC 480

QY 479 RGFYQDGRPGDRRAEKGPAKRTGQKWLDDLNKSENPRDLDLFLMAVLQNRHMATYFW 538
Db 481 RGFYQDGRPGDRRAEKGPAKRTGQKWLDDLNKSENPRDLDLFLMAVLQNRHMATYFW 540

QY 539 AWGEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECVSNSEARAFAL 598
Db 541 AWGEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECVSNSEARAFAL 600

QY 599 LVRRNRCSWTKTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAAGTPIILRLGAPLCPA 658
Db 601 LVRRNRCSWTKTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAAGTPIILRLGAPLCPA 660

QY 659 LVYTNLITFSBEAPLRTGLIEDLQDLSLDTKSPLYGLQSRVLELVEAPRAQSGRGPRAV 718
Db 661 LVYTNLITFSBEAPLRTGLIEDLQDLSLDTKSPLYGLQSRVLELVEAPRAQSGRGPRAV 720

QY 719 FLLTRWRKFWGAPVTVFLGNVMYFAFLFTYVLLVDFRPPPGPGSGPEVTLYFWVFTL 778
Db 721 FLLTRWRKFWGAPVTVFLGNVMYFAFLFTYVLLVDFRPPPGPGSGPEVTLYFWVFTL 780

QY 779 VLESTROGFFDDETHLVKFTLLVGNWNKCDMVAIFLFIIVGVTCTMLPSAFEAGRTVL 838
Db 781 VLESTROGFFDDETHLVKFTLLVGNWNKCDMVAIFLFIIVGVTCTMLPSAFEAGRTVL 840

QY 839 AMDPMVFTLRILHIFALHKLGPKEIIVVERMKDVPFFLPSVWLVAYGVTTQALLHPH 898
Db 841 AMDPMVFTLRILHIFALHKLGPKEIIVVERMKDVPFFLPSVWLVAYGVTTQALLHPH 900

QY 899 DGRLEWIFRVRVLPYLIQIFQIPLDEIDBARVNCSTHPLLEDSPSCPSLYANMLVILL 958
Db 901 DGRLEWIFRVRVLPYLIQIFQIPLDEIDBARVNCSTHPLLEDSPSCPSLYANMLVILL 960

QY 959 LVTFLVTVNLLMNLIIAMFSYTFQVVGNDMFKFQRYNLIVEYHERPALAPPFILLS 1018
Db 961 LVTFLVTVNLLMNLIIAMFSYTFQVVGNDMFKFQRYNLIVEYHERPALAPPFILLS 1020

QY 1019 HLSLTIRVFPKBAEHKREHLERDLPDLPDQKVVTWETQKENFLSKMKRRRDSSEVL 1078
Db 1021 HLSLTIRVFPKBAEHKREHLERDLPDLPDQKVVTWETQKENFLSKMKRRRDSSEVL 1080

QY 1079 RKTARHVDFTAKYLGRLGKREKRIKLESQINCSVLVSSVADVLAAQGGPRSSQHCSE 1138
Db 1081 RKTARHVDFTAKYLGRLGKREKRIKLESQINCSVLVSSVADVLAAQGGPRSSQHCSE 1140

QY 1139 SOLVAADHRGGLDQWGPQAGPPSDT 1165
Db 1141 SOLVAADHRGGLDQWGPQAGPPSDT 1167

RESULT 5

US-09-834-792-5
; Sequence 5, Application US/09834792
; Patent No. US20020037515A1
; GENERAL INFORMATION:
; APPLICANT: Mount Sinai School of Medicine of NYU
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
; TITLE OF INVENTION: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
; FILE REFERENCE: AP32911 070165.0589
; CURRENT APPLICATION NUMBER: US/09/834,792
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,491
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1164
; TYPE: PRT
; ORGANISM: Human
US-09-834-792-5

Query Match 99.4%; Score 6057.5; DB 9; Length 1164;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1161; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 MQDVQGPFGSGDADRELGHRGEVNFPGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
Db 1 MQDVQGPFGSGDADRELGHRGEVNFPGSGKRGKRVFVPSGVAPSVLFDLLAEW 60

QY 61 HLPAPNLVSLVGEQPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLRHVGQAV 120
Db 61 HLPAPNLVSLVGEQPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLRHVGQAV 120

QY 121 RDHSLASTTKRVVAVGMASLGRVLRHRLBEAQEDFPVHYPEDDGGSGGPLCSLDSNL 180
Db 121 RDHSLASTTKRVVAVGMASLGRVLRHRLBEAQEDFPVHYPEDDGGSGGPLCSLDSNL 180

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181 SHFVLVEPGPGKGDGLTELRLEKHSIQRAGYGGTSGSIEIPVLCVLLVNGDPTLRI 240
181 SHFVLVEPGPGKGDGLTELRLEKHSIQRAGYGGTSGSIEIPVLCVLLVNGDPTLRI 240
241 SRVVEQAAPWLLVSGGGIADVLAALVNQPHLLVPKVAEKQKPKFSPKSHFWSWEDIVRWT 300
241 SRVVEQAAPWLLVSGGGIADVLAALVNQPHLLVPKVAEKQKPKFSPKSHFWSWEDIVRWT 300
301 KLLQNTITSHOHLITVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDELKLA VADR 360
301 KLLQNTITSHOHLITVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDELKLA VADR 360
361 VDIKSEIFNGDVVEKSCDLEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOEL YR 420
361 VDIKSEIFNGDVVEKSCDLEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOEL YR 420
421 SVSRKSLFLDLLQRKQEEARLTLAGLGTQQAEPAPGPPAFSLHEVSRVLKDFLOD ACRG 480
421 SVSRKSLFLDLLQRKQEEARLTLAGLGTQQAEPAPGPPAFSLHEVSRVLKDFLOD ACRG 480
481 FYQDGRPGDGRRAEAKGPAKPTGQKWLDDLNOKSENPRDLFLMAVLQNRHEMATYFWAM 540
481 FYQDGRPGDGRRAEAKGPAKPTGQKWLDDLNOKSENPRDLFLMAVLQNRHEMATYFWAM 540
541 GOEGVAAALAAACKILKEMSHLEAEARATREAKYERLALDLFSECYSNSEARAFAL LV 600
541 GOEGVAAALAAACKILKEMSHLEAEARATREAKYERLALDLFSECYSNSEARAFAL LV 600
601 RNRNCSKTTTCLHLATEADAKAFPAHDGVQOAFETRIWGDMAAGTPIRLGLGAF LCPALV 660
601 RNRNCSKTTTCLHLATEADAKAFPAHDGVQOAFETRIWGDMAAGTPIRLGLGAF LCPALV 660
661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAGDGRGPRAV FL 720
661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAGDGRGPRAV FL 720
721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQPGSPGPEVTLFYFWFT LVL 780
721 LTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDPRPPQPGSPGPEVTLFYFWFT LVL 780
781 EIRQGFETDEDTHLVKKTFLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAFAGRTVLAM 840
781 EIRQGFETDEDTHLVKKTFLYVGDNNKCDMVAIFLFIIVGVTCTMLPSAFAGRTVLAM 840
841 DFVWFTLRLLHIFAIHKQGPKEIIVVERMMKDVFFFLFSLVNLVAYGVTTQALLHP HDG 900
841 DFVWFTLRLLHIFAIHKQGPKEIIVVERMMKDVFFFLFSLVNLVAYGVTTQALLHP HDG 900
901 RLEWIFRRVLYRPLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVL LVL 960
901 RLEWIFRRVLYRPLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVL LVL 960
961 TELLVNTNVLMLLIIAMESYTFQVQGNADMFWKFORYNLI VEYHERPALAPPFILL SHL 1020
961 TELLVNTNVLMLLIIAMESYTFQVQGNADMFWKFORYNLI VEYHERPALAPPFILL SHL 1020
1021 SLTLRRVFKKEAEHKEHLERDLDPDLDQKVVTWETVQKENFLSKMEKRRRDS EGEVLARK 1080
1021 SLTLRRVFKKEAEHKEHLERDLDPDLDQKVVTWETVQKENFLSKMEKRRRDS EGEVLARK 1080
1081 TAHRVDFIAKYLGLGLREQRIRIKLESQINYCSVLVSSVADVLAAQGGPRSSOHC EGSG 1140
1081 TAHRVDFIAKYLGLGLREQRIRIKLESQINYCSVLVSSVADVLAAQGGPRSSOHC EGSG 1140
1141 LVAADHRGGIDGWEOPGAGPPSDT 1165
1141 LVAADHRGGIDGWEOPGAGPPSDT 1165

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RESULT 6
US-10-794-897-7
; Sequence 7, Application US/10794897

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; Publication No. US20040259160A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Zhou, Yun-Ping
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes and Related Diseases Involving Beta-TRP
; FILE REFERENCE: 016325-019010US
; CURRENT APPLICATION NUMBER: US/10794.897
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/452,596
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human betaTRP (MBX) calcium channel
US-10-794-897-7

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Query Match 98.2%; Score 5985; DB 16; Length 1165;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 MODVQGPSPGPGDAEDRRRLGLHRGEVNFVGGSGKRGKGFVRVPSGVAPSVLFDLLAEW 60
DB 1 MODVQGPSPGPGDAEDRRRLGLHRGEVNFVGGSGKRGKGFVRVPSGVAPSVLFDLLAEW 60
QY 61 HLPAPNLVSVLVBEGEPFAMKSWLDRVLRKGLVKAQSTGAWILTSALRVGLARIVGQAV 120
DB 61 HLPAPNLVSVLVBEGEPFAMKSWLDRVLRKGLVKAQSTGAWILTSALRVGLARIVGQAV 120
QY 121 RDHSLASTSTKRVVAVGMAISLCRVLHRIIEEAQEDFPVHYPEDDGSGQGLCSLDSNL 180
DB 121 RDHSLASTSTKRVVAVGMAISLCRVLHRIIEEAQEDFPVHYPEDDGSGQGLCSLDSNL 180
QY 181 SHFVLVEPGPGKGDGLTELRLEKHSIQRAGYGGTSGSIEIPVLCVLLVNGDPTLRI 240
DB 181 SHFVLVEPGPGKGDGLTELRLEKHSIQRAGYGGTSGSIEIPVLCVLLVNGDPTLRI 240
QY 241 SRVVEQAAPWLLVSGGGIADVLAALVNQPHLLVPKVAEKQKPKFSPKSHFWSWEDIVRWT 300
DB 241 SRVVEQAAPWLLVSGGGIADVLAALVNQPHLLVPKVAEKQKPKFSPKSHFWSWEDIVRWT 300
QY 301 KLLQNTITSHOHLITVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDELKLA VADR 360
DB 301 KLLQNTITSHOHLITVYDFEQSGSEELDTVILKALVKACKSHSQEPQDYLDELKLA VADR 360
QY 361 VDIKSEIFNGDVVEKSCDLEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOEL YR 420
DB 361 VDIKSEIFNGDVVEKSCDLEEVMDALVSNKPEFVRLFVNDGADVADFLTYGRLOEL YR 420
QY 421 SVSRKSLFLDLLQRKQEEARLTLAGLGTQQAEPAPGPPAFSLHEVSRVLKDFLOD ACRG 480
DB 421 SVSRKSLFLDLLQRKQEEARLTLAGLGTQQAEPAPGPPAFSLHEVSRVLKDFLOD ACRG 480
QY 481 FYQDGRPGDGRRAEAKGPAKPTGQKWLDDLNOKSENPRDLFLMAVLQNRHEMATYFWAM 540
DB 481 FYQDGRPGDGRRAEAKGPAKPTGQKWLDDLNOKSENPRDLFLMAVLQNRHEMATYFWAM 540
QY 541 GOEGVAAALAAACKILKEMSHLEAEARATREAKYERLALDLFSECYSNSEARAFAL LV 600
DB 541 GOEGVAAALAAACKILKEMSHLEAEARATREAKYERLALDLFSECYSNSEARAFAL LV 600
QY 601 RNRNCSKTTTCLHLATEADAKAFPAHDGVQOAFETRIWGDMAAGTPIRLGLGAF LCPALV 660
DB 601 RNRNCSKTTTCLHLATEADAKAFPAHDGVQOAFETRIWGDMAAGTPIRLGLGAF LCPALV 660
QY 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAGDGRGPRAV FL 720
DB 661 YTNLITFSEAPLRTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAGDGRGPRAV FL 720

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QY 721 LTRWRKFWGAPVTVFLGNVVMYFAELFTVTVLLVDRPPQSGPSEVTLYFWVFTLV 780
DB 721 LTRWRKFWGAPVTVFLGNVVMYFAELFTVTVLLVDRPPQSGPSEVTLYFWVFTLV 780
QY 781 EEIRQGFTEDETHLVKKEFTLYVGNWNKCDMAIFLFIIVGVTCTMLPSAFAEAGRTVLAM 840
DB 781 EEIRQGFTEDETHLVKKEFTLYVGNWNKCDMAIFLFIIVGVTCTMLPSAFAEAGRTVLAM 840
QY 841 DFMVFTLRIHFAIKHQLGPKIIVVERMMKDVFFLFFLSVWLVAVGVTTOALLPHDQ 900
DB 841 DFMVFTLRIHFAIKHQLGPKIIVVERMMKDVFFLFFLSVWLVAVGVTTOALLPHDQ 900
QY 901 RLEWIFRRVLYRPLQIFGQIPLEIDIEARVNCSTHPLLEDSPCSLVANWLVILLV 960
DB 901 RLEWIFRRVLYRPLQIFGQIPLEIDIEARVNCSTHPLLEDSPCSLVANWLVILLV 960
QY 961 TFLVTVNVLNMLLIAMFSTFQVVOGNADMPKFORNLIIVYHERPALAPPFILLSHL 1020
DB 961 TFLVTVNVLNMLLIAMFSTFQVVOGNADMPKFORNLIIVYHERPALAPPFILLSHL 1020
QY 1021 SLTLRRVFKAEAKHREHLERDLPDLDQKVVTWETVQENFLSKMKRRRSEGEVLAK 1080
DB 1021 SLTLRRVFKAEAKHREHLERDLPDLDQKVVTWETVQENFLSKMKRRRSEGEVLAK 1080
QY 1081 TAHRVDFTIAXLGLRQEKRIKLESQINYSVLVSSVADVLAQGGPRSSQHCQGSQ 1140
DB 1081 TAHRVDFTIAXLGLRQEKRIKLESQINYSVLVSSVADVLAQGGPRSSQHCQGSQ 1140
QY 1141 LVAADHRGGLDGWEQPCAGQPPSDT 1165
DB 1141 LVAADHRGGLDGWEQPCAGQPPSDT 1165

RESULT 7

US-10-794-897-8
; Sequence 8, Application US/10794897
; Publication No. US20040259160A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Zhou, Yun-fang
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes and Related Diseases Involving Beta-TRP
; FILE REFERENCE: 016325-019010US
; CURRENT APPLICATION NUMBER: US/10/794,897
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/452,596
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: betaTRP sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)_
; OTHER INFORMATION: Xaa = Met, Thr or Asp
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)_
; OTHER INFORMATION: Xaa = Ala, Thr or Val
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (22)
; OTHER INFORMATION: Xaa = Val, Ile or Gly
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (46)

; OTHER INFORMATION: Xaa = Asn, Ser or Gly
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (156)
; OTHER INFORMATION: Xaa = Gln or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (157)
; OTHER INFORMATION: Xaa = Lys or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (170)
; OTHER INFORMATION: Xaa = Ser, Asn or Gly
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (171)
; OTHER INFORMATION: Xaa = Thr, Ile or Ser
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (192)
; OTHER INFORMATION: Xaa = Thr, Ala or Pro
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (271)
; OTHER INFORMATION: Xaa = Gly, Ser or Asn
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (459)
; OTHER INFORMATION: Xaa = Val, Ile or Ala
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (490)
; OTHER INFORMATION: Xaa = Pro or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (491)
; OTHER INFORMATION: Xaa = Gly or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (492)
; OTHER INFORMATION: Xaa = Asp or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (493)
; OTHER INFORMATION: Xaa = Arg or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (699)
; OTHER INFORMATION: Xaa = His, Arg or Leu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1140)
; OTHER INFORMATION: Xaa = Arg, Cys or Glu
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1151)..(1152)
; OTHER INFORMATION: Xaa = Gly or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1153)
; OTHER INFORMATION: Xaa = Leu or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1154)
; OTHER INFORMATION: Xaa = Asp or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1155)
; OTHER INFORMATION: Xaa = Gly or is absent
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1156)
; OTHER INFORMATION: Xaa = Trp or is absent

US-10-794-897-8

Query Match 84.3%; Score 5134.5; DB 16; Length 1168;
Best Local Similarity 84.8%; Pred. No. 0;
Matches 990; Conservative 61; Mismatches 114; Indels 3; Gaps 2;

QY 1 MODVGPDPGDAEDRRLGLHGEVNFVFGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
DB 1 MOXVSSCPGPPDTEGWEXLCEGVNFVFGSGKRGKRVFVPSGVAPSVLFDLLAEW 60

QY 61 HLPAPNLVSVLGEERPFAMKSWLRLVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
DB 61 HLPAPNLVSVLGEERPFAMKSWLRLVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120

QY 121 RDHSLASTSKRVVAVGASLGRVILHRRILEAQ--EDFPVHYVEDDGGSGPLCSLDS 178
DB 121 RDHSLASTSKRVVAVGASLGRVILHRRILEAQ--EDFPVHYVEDDGGSGPLCSLDS 180

QY 179 NLSHFILVEPGPGKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPVLCILVNGDPNTL 237
DB 181 NLSHFILVEPGVLSGNDGLTELQSLKHISQORTGYGGTSSIQIPVLCILVNGDPNTL 240

QY 238 ERISRAVEQAAPWLILVSGGGIADVLAALVNPHLLVPKVAEKQPKFPPSKHFSWEDIV 297
DB 241 ERISRAVEQAAPWLILVSGGGIADVLAALVNPHLLVPQVAEKQPREKFPSECFSEWAI 300

QY 298 RWTKLLQNTSHOHLTVYDFPEQSEELDTVILKALVKAKSHSQEPQDYLDLKLAVA 357
DB 301 HWTLLQNTIAAPHLLTVYDFPEQSEELDTVILKALVKAKSHSQEAQDYLDLKLAVA 360

QY 358 WDRVDIAKSEIENGVEWKSCLDEEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 417
DB 361 WDRVDIAKSEIENGVEWKSCLDEEVMVDALVSNKPEFVRLFVDSGADWAEFLTYGRLOQ 420

QY 418 LYRSVSRKSLLDLQRLQKQEARLTLAGLTQQAAREPPAGPPAFSLHVSRLVKDFLODA 477
DB 421 LYHSVSPKSLDFELLQRLKHEEGRLTLAGLGAQARELPXGLPAFSLHVSRLVKDFLHDA 480

QY 478 CRGFYODGRPGDRRAEKGPAPKPTQCKWLLDLNOKSENPDWDLFLWAVLQNRHEMATYF 537
DB 481 CRGFYODGRXXXRMEERPPKPPAGQKWLPLSRKSEDPWRDLFLWAVLQNRHEMATYF 540

QY 538 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYNSBARAPA 597
DB 541 WAMREGVAAALAAACKIILKEMSHLEKEAEVARTMREAKYTEQLALDLFSECYNSBARAPA 600

QY 598 LLVRRNCWKTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAGTPIRLLLGAFLCP 657
DB 601 LLVRRNHSRTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAGTPIRLLLGAFTCP 660

QY 658 ALVYTNLITFSEAPLRTGLELDLQDLSLDEKSPLYGLQSRVEELVEAPRAQDGRGPA 717
DB 661 ALITYTNLISFEDAPQMDLEDLQEPDLSLDEKSFCLSGGQLEKLEAPRAPGDLGPOA 720

QY 718 VELLTWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPPQSPGSEVTLTYEWVFT 777
DB 721 AFELLTWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPPQSPGSEVTLTYEWVFT 780

QY 778 LVLEERIQGFTEDETHLVKFTLYVGDNNWNCMDVAIFLIVGVTCRMLPSAFEAGRTV 837
DB 781 LVLEERIQGFTEDETHLVKFTLYVGDNNWNCMDVAIFLIVGVTCRWVPSVFEAGRTV 840

QY 838 LAMDPMVFTLRLIHFIAHKQLGPKIIVVERMKQDVFFFLFVSVMLVAYGVTTQALLHP 897
DB 841 LAIDPMVFTLRLIHFIAHKQLGPKIIVVERMKQDVFFFLFVSVMLVAYGVTTQALLHP 900

QY 898 HDGRLEWIFRVLRYRPLQIFGQIPLDEIDEARVNCSTHPELLEDSPCSLVANMLVIL 957
DB 901 HDGRLEWIFRVLRYRPLQIFGQIPLDEIDEARVNCSTHPELLEDSPCSLVANMLVIL 960

QY 958 LLVTFLVTNVLNMLLIAMFSYTFQVQGNADMFWKFORNLIIVEYHERPALAPPFILL 1017
DB 961 LLVTFLVTNVLNMLLIAMFSYTFQVQGNADMFWKFORNLIIVEYHERPALAPPFILL 1020

QY 1018 SHLSLTLRRVFKAEAEHREHLERDLDPDLQKVVTWETVQKENFLSKMRKRDRDSGEV 1077
DB 1021 SHLSVLVKQVRKEAQHQRHLERDLDPDLQKVVTWETVQKENFLSKMRKRDRDSGEV 1080

QY 1078 LRKTAHRVDIAKYGLGIREQEKRIKLESQINVCVSVLSSVADVLAOGGPRSSOHCGE 1137
DB 1081 LRKTAHRVDIAKYIGLIREQEKRIKLESQANVCMLLLSSMTDTLAPGGTYSSQNCGX 1140

QY 1138 GSQLVAAADHRGLDGEQPGAGQPPSDT 1165
DB 1141 RSQPASARDRXXXXXXEYLEAGLPPSDT 1168

RESULT 8
US-09-834-792-2
; Sequence 2, Application US/09834792
; Patent No. US20020037515A1
; GENERAL INFORMATION:
; APPLICANT: Mount Sinai School of Medicine of NYU
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
; TITLE OF INVENTION: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
; FILE REFERENCE: AP32911 070165 0589
; CURRENT APPLICATION NUMBER: US/09/834,792
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,491
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Murine TRP8
US-09-834-792-2

Query Match 83.5%; Score 5088.5; DB 9; Length 1158;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

QY 1 MODVGPDPGDAEDRRLGLHGEVNFVFGSGKRGKRVFVPSGVAPSVLFDLLAEW 60
DB 1 MOTTOSCPGPPDTEGWEXLCEGVNFVFGSGKRGKRVFVPSGVAPSVLFDLLAEW 60

QY 61 HLPAPNLVSVLGEERPFAMKSWLRLVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
DB 61 HLPAPNLVSVLGEERPFAMKSWLRLVLRKGLVKAQSTGAWILTSALRVGLARHVQAV 120

QY 121 RDHSLASTSKRVVAVGASLGRVILHRRILEAQ--EDFPVHYVEDDGGSGPLCSLDS 178
DB 121 RDHSLASTSKRVVAVGASLGRVILHRRILEAQ--EDFPVHYVEDDGGSGPLCSLDS 180

QY 179 NLSHFILVEPGPGKG-DGLTELRLRLEKHISEQAGYGGTGSIEIPVLCILVNGDPNTL 237
DB 181 NLSHFILVESGALSGNDGLTELQSLKHISQORTGYGGTSSIQIPVLCILVNGDPNTL 240

QY 238 ERISRAVEQAAPWLILVSGGGIADVLAALVNPHLLVPKVAEKQPKFPPSKHFSWEDIV 297
DB 241 ERISRAVEQAAPWLILVSGGGIADVLAALVNPHLLVPQVAEKQPREKFPSECFSEWAI 300

QY 298 RWTKLLQNTSHOHLTVYDFPEQSEELDTVILKALVKAKSHSQEPQDYLDLKLAVA 357
DB 301 HWTLLQNTIAAPHLLTVYDFPEQSEELDTVILKALVKAKSHSQEAQDYLDLKLAVA 360

QY 358 WDRVDIAKSEIENGVEWKSCLDEEVMVDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 417
DB 361 WDRVDIAKSEIENGVEWKSCLDEEVMVDALVSNKPEFVRLFVDSGADWAEFLTYGRLOQ 420

QY 418 LYRSVSRKSLLDLQRLQKQEARLTLAGLTQQAAREPPAGPPAFSLHVSRLVKDFLODA 477
DB 421 LYHSVSPKSLDFELLQRLKHEEGRLTLAGLGAQARELPXGLPAFSLHVSRLVKDFLHDA 480

QY 478 CRGFYODGRPGDRRAEKGPAPKPTQCKWLLDLNOKSENPDWDLFLWAVLQNRHEMATYF 537
DB 481 CRGFYODGRPGDRRAEKGPAPKPTQCKWLLDLNOKSENPDWDLFLWAVLQNRHEMATYF 537

Db 481 CRGYQDG-----RRMEERGPKPKAGQKWLPLSRKSDPWRDLFLMAVLQNRVEMATYF 536
 Qy 538 WAMGQGVAAALAAACKILKEMSHLETEAEARATREAKYERIALDLFSECVSNSEARAF 597
 Db 537 WAMRGVAAALAAACKILKEMSHLEKEAEAVARTREAKYEQALDLFSECVSNSEARAF 596
 Qy 598 LLVRRNRCSKTTCLHLATEADAKAFFAHGQVQAFLTRIWMCDMAAGTPIRLILGALCP 657
 Db 597 LLVRRNHSRRTTCLHLATEADAKAFFAHGQVQAFLTRIWMCDMAAGTPIRLILGALCP 656
 Qy 658 ALVYTNLITFSEAPLRTGLDQLDLSLDEKSPYGLQSRVBEELVEAPRAQDGRPA 717
 Db 657 ALIYTNLITFSEAPLRTGLDQLDLSLDEKSPYGLQSRVBEELVEAPRAQDGRPA 716
 Qy 718 VELLTRWRKFWGAPVTVFLGNVVMYFAFLFTVYLLVDRPPPPQSGSEVTLVFWVFT 777
 Db 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTVYLLVDRPPPPQSGSEVTLVFWVFT 776
 Qy 778 LVLEIRQGFTEDETHLVKKFTLYVGNMKNKCDMAIFLFIIVGVTCRMLPSFAEAGRTV 837
 Db 777 LVLEIRQGFTEDETHLVKKFTLYVGNMKNKCDMAIFLFIIVGVTCRMLPSFAEAGRTV 836
 Qy 838 LAMDPMVFTLRLIHFALHKLQPKIIVVERMKDVFVFLFSLVNLVAYGVTTQALLHP 897
 Db 837 LAIDPMVFTLRLIHFALHKLQPKIIVVERMKDVFVFLFSLVNLVAYGVTTQALLHP 896
 Qy 898 HDGRLWIFRVLRYPLQIPIQIPLDEIDEARVNCSTHPLLEDSPSPSLYANLVL 957
 Db 897 HDGRLWIFRVLRYPLQIPIQIPLDEIDEARVNCSTHPLLEDSPSPSLYANLVL 956
 Qy 958 LLVTFLLVTVNLLNLLIAMFSYTFVQVQGNADMFWKFORNLIYVYHERPALAPFFILL 1017
 Db 957 LLVTFLLVTVNLLNLLIAMFSYTFVQVQGNADMFWKFORNLIYVYHERPALAPFFILL 1016
 Qy 1018 SHLSLTLRRVFKAEHKEHLEERDLPDQKVVTWETVQKENFLSKWEKRRDSEGV 1077
 Db 1017 SHLSLTLRRVFKAEHKEHLEERDLPDQKVVTWETVQKENFLSKWEKRRDSEGV 1076
 Qy 1078 LRKTAHRVDVIAKVLGLRQEKRIKLESQINYSVLVSVADVLAQGGPRSSHQGE 1137
 Db 1077 LRKTAHRVDVIAKVLGLRQEKRIKLESQINYSVLVSVADVLAQGGPRSSHQGE 1136
 Qy 1138 GSQVLAADHGGDQWEGPQAGQPPSDT 1165
 Db 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 9

; US-10-026-188-5
 ; Sequence 5, Application US/10026188
 ; Publication No. US20020164645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Zhang, Yifeng
 ; TITLE OF INVENTION: The Regents of the University of California
 ; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
 ; TITLE OF INVENTION: Ion Channel
 ; FILE REFERENCE: 02307E-114910US
 ; CURRENT APPLICATION NUMBER: US/10/026.188
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: US 60/259,379
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 1158
 ; TYPE: PR1
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; OTHER INFORMATION: mouse ltrpc5 predicted amino acid sequence
 ; US-10-026-188-5

Query Match

83.5%; Score 5089.5; DB 13; Length 1158;

Best Local Similarity 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

Qy 1 MODVQPPGSGDAEDRRRLGLHRRGEVNFSGSKKGGKVRVPVSGVAPVLPDLLAEW 60
 Db 1 MQTQSSCPGPPDTEDEWEIFLCRGEINFGSGKGGKFKVPSSVAPVLPFELLTEW 60
 Qy 61 HLPAPNLVVLVBGEQPPFAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
 Db 61 HLPAPNLVVLVBGEQPPFAMKSWLRDLVRKGLVKAQSTGAWILTSALRVGLARHVQAV 120
 Qy 121 RDHSLASTSTKRVVAVVAVMASLGRVLRHRTLE--EAQEDPPVHYPPDDGSGQSPCLSDS 178
 Db 121 RDHSLASTSTKRVVAVVAVMASLGRVLRHRTLE--EAQEDPPVHYPPDDGSGQSPCLSDS 178
 Qy 179 NLSHFILVPEPPGKG-DGTELRLEKHSIQRAGYGGTGTGSIETPIVLCVLVNGDPNTL 237
 Db 181 NLSHFILVPEPPGKG-DGTELRLEKHSIQRAGYGGTGTGSIETPIVLCVLVNGDPNTL 240
 Qy 238 ERISRAVEQAAPMLILVSGGIADVLAAVNVQPHLLVPKVAEKQPKPKPSPKHFWMEDIV 297
 Db 241 ERISRAVEQAAPMLILVSGGIADVLAAVNVQPHLLVPKVAEKQPKPKPSPKHFWMEDIV 297
 Qy 298 RWTKLQNTSHOHLTVYDFEQEGSEELDTVLKALVKACKSHSQEADQYLDLKLAVA 357
 Db 301 HWTQLQNTSHOHLTVYDFEQEGSEELDTVLKALVKACKSHSQEADQYLDLKLAVA 360
 Qy 358 WDRVDIAKSIIFNGDVWEKSCDLEEVMDALVSNKPEFVRLVFNAGVADVPDLYGRLOE 417
 Db 361 WDRVDIAKSIIFNGDVWEKSCDLEEVMDALVSNKPEFVRLVFNAGVADVPDLYGRLOE 420
 Qy 418 LYRSVRSKSLFDLQKQKEARLTLAGLGTQQAEPPEPPAPFSLHVSRLVLDPLODA 477
 Db 421 LYRSVRSKSLFDLQKQKEARLTLAGLGTQQAEPPEPPAPFSLHVSRLVLDPLODA 480
 Qy 478 CRGYQDGPGDPRRAEAKGPAKPTGQKWLDLNOKSNPWRDLFLMAVLQNRHEMATYF 537
 Db 481 CRGYQDGPGDPRRAEAKGPAKPTGQKWLDLNOKSNPWRDLFLMAVLQNRHEMATYF 536
 Qy 538 WAMGQGVAAALAAACKILKEMSHLETEAEARATREAKYERIALDLFSECVSNSEARAF 597
 Db 537 WAMGQGVAAALAAACKILKEMSHLETEAEARATREAKYERIALDLFSECVSNSEARAF 596
 Qy 598 LLVRRNRCSKTTCLHLATEADAKAFFAHGQVQAFLTRIWMCDMAAGTPIRLILGALCP 657
 Db 597 LLVRRNHSRRTTCLHLATEADAKAFFAHGQVQAFLTRIWMCDMAAGTPIRLILGALCP 656
 Qy 658 ALVYTNLITFSEAPLRTGLDQLDLSLDEKSPYGLQSRVBEELVEAPRAQDGRPA 717
 Db 657 ALIYTNLITFSEAPLRTGLDQLDLSLDEKSPYGLQSRVBEELVEAPRAQDGRPA 716
 Qy 718 VELLTRWRKFWGAPVTVFLGNVVMYFAFLFTVYLLVDRPPPPQSGSEVTLVFWVFT 777
 Db 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTVYLLVDRPPPPQSGSEVTLVFWVFT 776
 Qy 778 LVLEIRQGFTEDETHLVKKFTLYVGNMKNKCDMAIFLFIIVGVTCRMLPSFAEAGRTV 837
 Db 777 LVLEIRQGFTEDETHLVKKFTLYVGNMKNKCDMAIFLFIIVGVTCRMLPSFAEAGRTV 836
 Qy 838 LAMDPMVFTLRLIHFALHKLQPKIIVVERMKDVFVFLFSLVNLVAYGVTTQALLHP 897
 Db 837 LAIDPMVFTLRLIHFALHKLQPKIIVVERMKDVFVFLFSLVNLVAYGVTTQALLHP 896
 Qy 898 HDGRLWIFRVLRYPLQIPIQIPLDEIDEARVNCSTHPLLEDSPSPSLYANLVL 957
 Db 897 HDGRLWIFRVLRYPLQIPIQIPLDEIDEARVNCSTHPLLEDSPSPSLYANLVL 956
 Qy 958 LLVTFLLVTVNLLNLLIAMFSYTFVQVQGNADMFWKFORNLIYVYHERPALAPFFILL 1017
 Db 957 LLVTFLLVTVNLLNLLIAMFSYTFVQVQGNADMFWKFORNLIYVYHERPALAPFFILL 1016
 Qy 1018 SHLSLTLRRVFKAEHKEHLEERDLPDQKVVTWETVQKENFLSKWEKRRDSEGV 1077

Db 1017 SHLSVLVQVFRKBAHQKRLERDLPDLPDQKIITWETQKCNFLSTMKRRRSEGEV 1076
Qy 1078 LRKTAHRVDFTAKYLGGLREGEKRIKLESQINYSVLVSSVADVLAQGGGPRSSOHGCE 1137
Db 1077 LRKTAHRVDLTAKYTGGREGEKRIKLESQANYSMLLSMTDTPLAGGYTSSQNCGC 1136
Qy 1138 GSQLVAADHRGGLDGEQPGAGQPPSDT 1165
Db 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 10
US-10-794-897-4
; Sequence 4, Application US/10794897
; Publication No. US20040259160A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Zhou, Yun-Ping
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes and Related Diseases Involving Beta-TRP
; FILE REFERENCE: 016325-019010US
; CURRENT APPLICATION NUMBER: US/10/794,897
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/452,596
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse betaTRP (TRPM5) calcium channel
US-10-794-897-4

Query Match 83.5%; Score 5088.5; DB 16; Length 1158;
Best Local Similarity, 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;

Qy 1 MDVQGPSPGDAEDRELGLHGEVNFSGGKRGKFKVRVPSGVAPSVLPDLLLLAPW 60
Db 1 MQTQSSCGSPDTEGWEPILCRGEINFGSGKRGKFKVRVPSGVAPSVLPFELLTEW 60
Qy 61 HLPAPNLVSLVGEOPFAMKSWLRDLVRKGLVKAQSTGAMILTSALVGLARHVQAV 120
Db 61 HLPAPNLVSLVGEERPLAMKSWLRDLVRKGLVKAQSTGAMILTSALVGLARHVQAV 120
Qy 121 RDSLASTTKVRVAVGWSLGRVLRHRIE--EAQEDFPVHYREDGSGSQPLCSLDS 178
Db 121 RDSLASTTKIRVVAIGMSLDRIILHRLQDLGVHOKEDTPHYPADENIOGPLCPLDS 180
Qy 179 NLSHFTLVPPGPKG-DGLTELRLKLEHISQRAGYGTGSIETPVLCLLVNGDPNTL 237
Db 181 NLSHFTLVPSGALSGNDGLTELQLSLEKHSIQRTGYGTGSIQIPVLCLLVNGDPNTL 240
Qy 238 ERISRAVEQAAPMLILVSGGIDVLAALVNPHLLVPKVAEKQFKKEPPSKHPSHWEDIV 297
Db 241 ERISRAVEQAAPMLILAGSGGIADVLAALVSPHLLVPQVAEKQFKKEPPSECFSEWATV 300
Qy 298 RWTKLQNTSHOHLTVYDFEAGSEEDTLTKALVKACKSHSOEPDYLDELKLA 357
Db 301 HWTELLQNTAAHPHLLTVYDFEAGSEEDTLTKALVKACKSHSOEAQDYLDELKLA 360
Qy 358 WDRVDIAKSIENGVDVWKSCLDEEVNVDALVSNKPEFVRLFDVNGADVADFLTYGRLOE 417
Db 361 WDRVDIAKSIENGVDVWKSCLDEEVNMTDALVSNKPEFVRLFDVSDGADWAEFLTYGRLOE 420
Qy 418 LYRSVSRKSLFLDLQKQKQEARLTLAGTQQAQRPAPAPAFSLHVSRLVKDFLQDA 477
Db 421 LYHSVSPKSLFLDLQKQKQEARLTLAGTQQAQRELPIGLPAPAFSLHVSRLVKDFLQDA 480
Qy 478 CRGFYQDGRGDRRAEKGPAKPTGQKWLDDLQKSENPRDLFLWAVLQNRHEMATYF 537

Db 481 CRGFYQDQ-----RMEERGGPKRPAQKWLDPDLSRKSDEDPWRDLFLWAVLQNRHEMATYF 536
Qy 538 WAMQOEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECVSNSEARAF 597
Db 537 WAMQOEGVAAALAAACKILKEMSHLEKEAEVARTWEAKYERLALDLFSECVSNSEARAF 596
Qy 598 LLVRNRCWSKTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPIRLILGAFCLP 657
Db 597 LLVRNHSWRTTCLHLATEADAKAFPAHDGVQAFLTRIWMGDMAAGTPIRLILGAFCLP 656
Qy 717 ALVVTNLTSEEAPLRTGLDLDLQDLSLDEKSPLYGLOSREVEELVEAPRAQDGRGPA 717
Db 657 ALIYTNLISFSEDAPQMDLEDLQEPDLSLDEKSPLYGLOSREVEELVEAPRAQDGRGPA 716
Qy 718 VFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPGSGSEVTLYFWYFT 777
Db 717 AFLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQPGSGSEVTLYFWYFT 776
Qy 778 LVLBEIRQGFPTDTHLVKKFTLYVGNMNMKDMVAIFLFIIVGTCMLSPSAFEAGRTV 837
Db 777 LVLBEIRQGFPTDTHLVKKFTLYVGNMNMKDMVAIFLFIIVGTCMLSPSAFEAGRTV 836
Qy 838 LAMDPMVFTLRIHFAHKOLGPKLIIVBERMKDVFELFELSVLWVAYGVTTQALLHP 897
Db 837 LAIDFMVFTLRIHFAHKOLGPKLIIVBERMKDVFELFELSVLWVAYGVTTQALLHP 896
Qy 898 HDGRLEWIFRVLVRYLPYQIFGOIPDLDEIDARVNCSTHPLLEDSPSCPSLYANLWVIL 957
Db 897 HDGRLEWIFRVLVRYLPYQIFGOIPDLDEIDARVNCSTHPLLEDSPSCPSLYANLWVIL 956
Qy 958 LLVTFLLVTNVLNMLLIAMFSYTFQVVGQNMDFKQRYNLIIVYHERPALAPPFILL 1017
Db 957 LLVTFLLVTNVLNMLLIAMFSYTFQVVGQNMDFKQRYNLIIVYHERPALAPPFILL 1016
Qy 1018 SHLSJTLRVRPKKAEHREHLERDLPDLPDQKVVWTWETQKCNFLSTMKRRRSEGEV 1077
Db 1017 SHLSJTLRVRPKKAEHREHLERDLPDLPDQKVVWTWETQKCNFLSTMKRRRSEGEV 1076
Qy 1078 LRKTAHRVDFTAKYLGGLREGEKRIKLESQINYSVLVSSVADVLAQGGGPRSSOHGCE 1137
Db 1077 LRKTAHRVDLTAKYTGGREGEKRIKLESQANYSMLLSMTDTPLAGGYTSSQNCGC 1136
Qy 1138 GSQLVAADHRGGLDGEQPGAGQPPSDT 1165
Db 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 11
US-10-794-897-6
; Sequence 6, Application US/10794897
; Publication No. US20040259160A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Zhou, Yun-Ping
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes and Related Diseases Involving Beta-TRP
; FILE REFERENCE: 016325-019010US
; CURRENT APPLICATION NUMBER: US/10/794,897
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/452,596
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1156
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat betaTRP calcium channel
US-10-794-897-6

```
Query Match      82.5%; Score 5025.5; DB 16; Length 1156;
Best Local Similarity 83.0%; Pred. No. 0;
Matches 968; Conservative 75; Mismatches 112; Indels 11; Gaps 3;

QY 1 MDVQGPDPGSDAERRELGHRVNFVGGSGKRGKRVVPVSGVAPSVLFDLLAEW 60
DB 1 MPMAQSSCPGPPDTGDNWEPVLCCKGBVNFVGGSGKSKVKVPSNVAPSMLELLTETW 60
QY 61 HLPAPNLVSVLVGSEPPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLARHVQAV 120
DB 61 HLPAPNLVSVLVGSEPPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLARHVQAV 120
QY 121 RDHSLASTSTKVRVAVGMSASGRVLRHRLLEKHSIQRTGYGTTSSIQIPVLCVNGDPSTLER 239
DB 121 RDHSLASTSTKVRVAVGMSASGRVLRHRLLEKHSIQRTGYGTTSSIQIPVLCVNGDPSTLER 239
QY 181 SHFLLVPEPPGKG-DGLTELRLRLKHSIQRTGYGTTSSIQIPVLCVNGDPSTLER 248
DB 181 SHFLLVPEPPGKG-DGLTELRLRLKHSIQRTGYGTTSSIQIPVLCVNGDPSTLER 248
QY 240 ISRAVEQAAPWLLVSGGGIADVLAAALVNOPHLLVPKVAEKQKPKFSPKSHFSDIWRM 299
DB 241 MSRAVEQAAPWLLVSGGGIADVLAAALVNOPHLLVPKVAEKQKPKFSPKSHFSDIWRM 299
QY 300 TKLLQNTSHOHLTVYDFEQSGSELDVTILKALVKACKSHSQEPQDYLDLKLAVWD 359
DB 301 TELLQNTIAHPHLLTVYDFEQSGSELDVTILKALVKACKSHSQEPQDYLDLKLAVWD 360
QY 360 RVDIAKSEIFNGDVENKSCDLEEVMTDALVSNKPEFVRLFDVNGADVADFTYGRLOELY 419
DB 361 RVDIAKSEIFNGDVENKSCDLEEVMTDALVSNKPEFVRLFDVNGADVADFTYGRLOELY 420
QY 420 RSVSRKSLFLDLQKQKQBEARLTLAGLGTQQAEPFAPAFSHSVRLKQFLODADR 479
DB 421 HSVSPKSLFLDLQKQKQBEARLTLAGLGTQQAEPFAPAFSHSVRLKQFLODADR 480
QY 480 GFYQDGRPRDRAEKGPAKRTGQKWLDDNOKSENPRDILFWAVLQNRHEMATYFWA 539
DB 481 GFYQDGRPRDRAEKGPAKRTGQKWLDDNOKSENPRDILFWAVLQNRHEMATYFWA 536
QY 540 MQQGVAAALAAKILKEMSHLETAEEAARAFAKRYERLALDLFSECVSNSEARAFALL 599
DB 537 MGREGVAAALAAKILKEMSHLETAEEAARAFAKRYERLALDLFSECVSNSEARAFALL 596
QY 600 VRNRCSWSTTCLHATEADAKAFPAHDGVQAFPLRIWGDMAAGTPTILRLGAGLCPAL 659
DB 597 VRNRCSWSTTCLHATEADAKAFPAHDGVQAFPLRIWGDMAAGTPTILRLGAGLCPAL 656
QY 660 VYTNLITFSEAPRLTGLDQLDLSLDEKSPVLYGLQSRVEELVEAPRAQDGRPAVF 719
DB 657 VYTNLITFSEAPRLTGLDQLDLSLDEKSPVLYGLQSRVEELVEAPRAQDGRPAVF 716
QY 720 LLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFPRPPQPGSPGSEVTLFWFVTLV 779
DB 717 LLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFPRPPQPGSPGSEVTLFWFVTLV 776
QY 780 LEEIRQGFTEDETHLVKFKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAPAGRTVLA 839
DB 777 LEEIRQGFTEDETHLVKFKFTLYVGDNNKCDMVAIFLIVGVTCRMLPSAPAGRTVLA 836
QY 840 MDMVFTLRLIHI FAIHKQLGPKIIVVERMMKDVFFFLFVSLVVAIVGVTQALLHPHD 899
DB 837 IDFMVFTLRLIHI FAIHKQLGPKIIVVERMMKDVFFFLFVSLVVAIVGVTQALLHPHD 896
QY 900 GRLEWIFRVLRYRPLQIFQGIPLDEIDEARVNGSTHPLLEDSPSCPSIYANWLVILL 959
DB 897 GRLEWIFRVLRYRPLQIFQGIPLDEIDEARVNGSTHPLLEDSPSCPSIYANWLVILL 956
QY 960 VTFLLVTVNLLMNLIIAMFSYTFVQGNADMFVKFORNLIYVEYHERPALAPFTLLSH 1019
DB 957 VTFLLVTVNLLMNLIIAMFSYTFVQGNADMFVKFORNLIYVEYHERPALAPFTLLSH 1016
QY 1020 LSLTLRRVFKAEHKEHLEHRLDPLDQKVTVTWETVQKENFSLKMKERRRDESEVL 1079
DB 1017 LSLTLRRVFKAEHKEHLEHRLDPLDQKVTVTWETVQKENFSLKMKERRRDESEVL 1076
QY 1080 KTAHRVDIAKYIGLREQEKRIKLESQINYSVSVVADVLAQGGPRSSQHCCEGS 1139
DB 1077 KTAHRVDIAKYIGLREQEKRIKLESQINYSVSVVADVLAQGGPRSSQHCCEGS 1136
QY 1140 QLVAAHRRGLDGEQPCAGOPPSDT 1165
DB 1137 QPASARDREYLE-----AGLPHSDT 1156

RESULT 12
US-10-026-188-2
; Sequence 2, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yifeng
; APPLICANT: Zuker, Charles S.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat L-TRP taste predicted protein
US-10-026-188-2

Query Match      82.2%; Score 5008.5; DB 13; Length 1165;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 965; Conservative 77; Mismatches 113; Indels 11; Gaps 3;

QY 1 MDVQGPDPGSDAERRELGHRVNFVGGSGKRGKRVVPVSGVAPSVLFDLLAEW 60
DB 9 MPMAQSSCPGPPDTGDNWEPVLCCKGBVNFVGGSGKSKVKVPSNVAPSMLELLTETW 68
QY 61 HLPAPNLVSVLVGSEPPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLARHVQAV 120
DB 69 HLPAPNLVSVLVGSEPPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRVGLARHVQAV 128
QY 121 RDHSLASTSTKVRVAVGMSASGRVLRHRLLEKHSIQRTGYGTTSSIQIPVLCVNGDPSTLER 180
DB 129 RDHSLASTSTKVRVAVGMSASGRVLRHRLLEKHSIQRTGYGTTSSIQIPVLCVNGDPSTLER 188
QY 181 SHFLLVPEPPGKG-DGLTELRLRLKHSIQRTGYGTTSSIQIPVLCVNGDPSTLER 239
DB 189 SHFLLVPEPPGKG-DGLTELRLRLKHSIQRTGYGTTSSIQIPVLCVNGDPSTLER 248
QY 240 ISRAVEQAAPWLLVSGGGIADVLAAALVNOPHLLVPKVAEKQKPKFSPKSHFSDIWRM 299
DB 249 MSRAVEQAAPWLLVSGGGIADVLAAALVNOPHLLVPKVAEKQKPKFSPKSHFSDIWRM 308
QY 300 TKLLQNTSHOHLTVYDFEQSGSELDVTILKALVKACKSHSQEPQDYLDLKLAVWD 359
DB 309 TELLQNTIAHPHLLTVYDFEQSGSELDVTILKALVKACKSHSQEPQDYLDLKLAVWD 368
QY 360 RVDIAKSEIFNGDVENKSCDLEEVMTDALVSNKPEFVRLFDVNGADVADFTYGRLOELY 419
DB 369 RVDIAKSEIFNGDVENKSCDLEEVMTDALVSNKPEFVRLFDVNGADVADFTYGRLOELY 428
QY 420 RSVSRKSLFLDLQKQKQBEARLTLAGLGTQQAEPFAPAFSHSVRLKQFLODADR 479
DB 429 HSVSPKSLFLDLQKQKQBEARLTLAGLGTQQAEPFAPAFSHSVRLKQFLODADR 488
```

QY 480 GFYQGRPGDRERRAKGPAKRTGOKWLLDLNOKSENPRDLFLWAVLQNRHEMATYFWA 539
DB 489 GFYQGRPGDRERRAKGPAKRTGOKWLLDLNOKSENPRDLFLWAVLQNRHEMATYFWA 544
QY 540 MQQGVAAALAAACKILKEMSHLETAEAAARATREAKYERLALDLFSECYSENSEARAFALL 599
DB 545 MGRGVAAALAAACKILKEMSHLEAEAVARTREAKYEQALDLFSECYSENSEARAFALL 604
QY 600 VRRNRCWKTCTCHLATEADAKAFPAHDGVQVFLTRIWMGDMAAGTPIRLILGAFCLPAL 659
DB 605 VRRNHSWRTCTCHLATEADAKAFPAHDGVQVFLTRIWMGDMAAGTPIRLILGAFCLPAL 664
QY 660 VYTNLITSEAPLRTGLDLQDLSLDEKSPLYGLOSRLVEELVEAPRAQDGRPAVAF 719
DB 665 IYTNLITSEAPLRTGLDLQDLSLDEKSPLYGLOSRLVEELVEAPRAQDGRPAVAF 724
QY 720 LTRWRKFWGAPVTVFLGNVVMYFAPLFTYVLLVDFRPPQPGSGSEVTLTYFWVFTLV 779
DB 725 LTRWRKFWGAPVTVFLGNVVMYFAPLFTYVLLVDFRPPQPGSGSEVTLTYFWVFTLV 784
QY 780 LEEIRQGFPTDDETHLVKFTLYVGNWNNKCDMAIFLPIVGVTCRMLPSAFAEAGRTVLA 839
DB 785 LEEIRQGFPTDDETHLVKFTLYVGNWNNKCDMAIFLPIVGVTCRMLPSAFAEAGRTVLA 844
QY 840 MPMVFTLRLIHFALHKGOLPKIIVRRMKDVPFFLFLSVLWLVAYGVTTQALLPHD 899
DB 845 IDPMVFTLRLIHFALHKGOLPKIIVRRMKDVPFFLFLSVLWLVAYGVTTQALLPHD 904
QY 900 GRLEWIFRVLRYPLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILL 959
DB 905 GRLEWIFRVLRYPLQIFQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANWLVILL 964
QY 960 VTFLVNTVLLNMLLIAMSYTFQVQGNADMFQKQRYVHLLIVEYHGRPALAPPPTLLSH 1019
DB 965 VTFLVNTVLLNMLLIAMSYTFQVQGNADMFQKQRYVHLLIVEYHGRPALAPPPTLLSH 1024
QY 1020 LSLTLRRVFKGAHKEHLEHRLDPLDQKVVTWETVQENFLSMKRRRDSSEVL 1079
DB 1025 LSLTLRRVFKGAHKEHLEHRLDPLDQKVVTWETVQENFLSMKRRRDSSEVL 1084
QY 1080 KTAHRVDFAKYLGLLEQEKRIKLESQINVCYLSSVADVLAQGGPRSSQHCCEGS 1139
DB 1085 KTAHRVDFAKYLGLLEQEKRIKLESQINVCYLSSVADVLAQGGPRSSQHCCEGS 1144
QY 1140 QLVADHRGGLDQWEPGAGQPPSDT 1165
DB 1145 QPASARDREYLE-----AGLPHSDT 1164

RESULT 13
US-10-295-027-558
; Sequence 558, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 558
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-558

Query Match 40.2%; Score 2448.5; DB 15; Length 1166;
Beat Local Similarity 45.6%; Pred. No. 1.5e-202;
Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;

QY 26 GEVPPGSGKRGKVRVPSVAPSVLFDLLAEHHLAPNLVSLVSGEQQFAMKSWLR 85
DB 28 GELDTGAGKXSHNSLDRTPAAVYSLVTRTWGFRAPNLVSLVSGGSGFVLTWLQ 87
QY 86 DVLRGLVKAQSTGAWILTSLARVGLARHVGQAVRDHSLASTSTKVRVAVGMAISLGRV 145
DB 88 DLLRGLVRAQSTGAWIVTGLTGHGRHVAVRDHMASTG-GTKVAVGVPWGVV 146
QY 146 LHRRLILEBAQEDFPVHY-----PEDDGGSGQLCSLDSNLSHFILVEPPGPKGDLTEL 200
DB 147 RNRDLINPKGSFPARYWRGDPED--GVQFP--LDNYSAFFLVDDGTHGCLGGENRF 201
QY 201 RLRLKHXISEQAGYGGTGSIEIPVCLLVNDGPNLTERISRAVEQAAFWLLVSGGTA 260
DB 202 RLRLSEYISQOCTGVGGTG-IDIPVLLLIIDGDKMLTRINATQALPCLLVAGSGAA 260
QY 261 DVLAALVNPQLLVP-----KVAEQFKKFPSPKHSFWSMEDIVRWTKLLQNTSHOHL 313
DB 261 DCLAETLED--TLAPGSGGARQGEARDRIIRFPFK-----GDLEVLQAOVERIMTRKELL 313
QY 314 TVYDFEQSGSEHLDTVILKALVKACKSHSQEPQDYLDELKLAVAWDRVDIAKSEIFNGDV 373
DB 314 TVYSSE-DGSEEFIVLKVAC--GSSEASAVLDELRLAVANWVVDIAQSELPRGDI 370
QY 374 EWKSCDLEVMVDALVSNKPEFVFLVNDGADVADFLTYGRLOELYRSVRKSLFLDLQ 433
DB 371 QWRSPHLEASLMDALLNDPREFVRLIISHGLSHGLFTPMRLAQYLSAAPSNSLRNLD 430
QY 434 RKQEARLUTLAGL--GTQQAAREPPAGPPAFSLHESVRLKDFLQDACRFYQDGRGDRR 491
DB 431 QASHSAGTKAPALKGGAELRPP-----DVGHVLRMLLKGKVCAPRYPSGGGAWDPH 480
QY 492 RAEKGPAPKPTQKWLMLDLNOKS-----ENPWRDLFLWAVLQNRHEMATYFWAMGQ 542
DB 481 -----PGQFGESWYLLSKATSPSLDAGLQAPWSDLLWALLNRAQMAFYFWMGMS 535
QY 543 EGVAAALAAACKILKEMSHLETAEAAARATREA--KYTERLALDLFSSCYSENSEARAFALL 600
DB 536 NAVSSALGACLLLRVWARLEPDAEEAARRKDLAFEGMGVDLFGECYRSSEVRAARLL 595
QY 601 RNRWCWKTCTCHLATEADAKAFPAHDGVQVFLTRIWMGDMAAGTPIRLILGAFCLPAL 660
DB 596 RRCPLMGDATCQLAMQADARAFFAQDGVQSLTQKWMGDMASTTPIWLVALVAFPCPLI 655

[illegible]

RESULT 15

REF ID: A66587
US-10-142-649-2

US-10-142-043-Z
: Sequence 2. Application US/10142649

: Publication No. IIS20030143557A1

: GENERAL INFORMATION:

; GENERAL INFORMATION:
: APPLICANT: Penner Reinhold

APPLICANT: PENNER, REINHOLD
TITLE OF INVENTION: Methods of screening for TRPM4b Modulators

; TITLE OF INVENTION: METHODS OF SCREENING
; FILE REFERENCE: A-71225-2/PET/NRC

FILE REFERENCE: A-71325-2/RFT/NBC
CURRENT ASSOCIATION NUMBER: U8/10/113 648

; CURRENT APPLICATION NUMBER: US/10020002

; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 506251 938

60/30

; PRIOR FILING DATE: 2002-

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: P

; SEQ ID NO 2

; LENGTH: 12

; TYPE: PRT

; ORGANISM: HCO

Query Match	40.2%	Score	2448.5	DB 14	Length	1214
Best Local Similarity	45.6%	Pred. No.	1.6e-202			
Matches 534	Conservative	177	Mismatches	350	Indels	111
					Gaps	26

Search completed: June 22, 2005, 18:33:14
Job time : 183 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2005, 18:08:59 ; Search time 50 seconds
(without alignments)
2241.851 Million cell updates/sec

Title: US-09-834-792D-4
Perfect score: 6093
Sequence: 1 MQDVQPRPGSGDAERRE.....HRGLDQWQPGAGQPPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1134.5	18.6	488	JC7995	transient receptor
2	1070.5	17.6	1868	T23707	hypothetical prote
3	1000	16.4	1400	T22644	hypothetical prote
4	889	14.6	1707	T18951	hypothetical prote
5	326.5	5.4	1275	JU0092	trp protein - frui
6	317.5	5.2	1274	JN0015	trp protein - frui
7	294	4.8	1418	S40764	hypothetical prote
8	266.5	4.4	1124	JH0588	calmodulin-binding
9	247	4.1	899	F88391	protein R06B10.4
10	235.5	3.9	823	S44873	ZC21.2 protein - C
11	192	3.2	828	JC5807	trp3 protein - rat
12	176.5	2.9	793	S68238	trp1 protein - hu
13	176.5	2.9	810	T38361	TRPC1 protein - hu
14	165	2.7	823	T34472	hypothetical prote
15	164.5	2.7	3678	S28912	dystrophin - mouse
16	160.5	2.6	482	S61648	probable membrane
17	146	2.4	725	JC7531	calcium transport
18	145.5	2.4	675	T20822	hypothetical prote
19	144.5	2.4	839	JC7621	capsaicin receptor
20	139	2.3	727	JC7796	epithelial calcium
21	132	2.2	790	T20312	hypothetical prote
22	130	2.1	838	T20954	capsaicin receptor
23	130	2.1	2049	T43161	sodium channel pro
24	128	2.1	723	JC7795	epithelial calcium
25	128	2.1	900	T33026	hypothetical prote
26	124.5	2.0	608	G02640	polycystic kidney
27	123.5	2.0	1199	T37561	probable transcrip
28	123	2.0	1060	S63993	acrosomal protein
29	123	2.0	1075	T45570	kinesin-like prote

ALIGNMENTS

RESULT 1
JC7995

transient receptor potential-melastatin 4 channel - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Nov-2003 #sequence_revision 10-Nov-2003 #text_change 24-Nov-2003

C:Accession: JC7995

R:Murakami, M.; Xu, F.; Miyoshi, I.; Sato, E.; Ono, K.; Iijima, T.

Biochem. Biophys. Res. Commun. 307, 522-528, 2003

A:Title: Identification and characterization of the murine TRPM4 channel.

A:Reference number: JC7995; PMID:12893253

A:Accession: JC7995

A:Molecule type: DNA

A:Residues: 1-488 <MUR>

A:Cross-references: GB:NM000319

A:Experimental source: Brain, C57/BL6

C:Comment: This protein, a member of subfamily of transient receptor potential channels

C:Genetics:

A:Gene: trpm4

A:Map position: 7B2

A:Introns: 12/2; 153/2; 197/3; 256/1; 315/2; 384/1; 428/2; 452/3

C:Keywords: calcium entry; transient receptor potential; transmembrane domain; TRPM

Query Match 18.6%; Score 1134.5; DB 2; Length 488;
Best Local Similarity 47.6%; Pred. No. 1.6e-74;
Matches 236; Conservative 72; Mismatches 123; Indels 65; Gaps 10;

Qy	704	VEAPRAQGRGPRAVF---	LLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPP	760
Db	20	VALERRQRPRGALCCGKFSKRWSDFWGAPVTAFLGNVSYLLFLLFAHLLVDFQPT	79	
Qy	761	POGSPGPEVTLYFWVFTLVLEIRQGF-----	PTDEDTHLVKKFTLYLVGDNNWK	809
Db	80	K--PSVSELLLYFWAFTLCEELRQGLGGWGSGLASGGRGPDAPLRHRLHLYLSDTNQ	137	
Qy	810	CDWVAIFLPIVGVTCRMLPSAFEGARTVLAMD	FMVFTLRLIHI FAIHKQLGPKIIVVERM	869
Db	138	CDLLALTCFLGVGCELTGLDGLTVLCLDFMIFTLLHFTVWKQLGPKIVIVSKM	197	
Qy	870	MKDVFVFFFLSVMLVAVGVTTOALLPHDGRLEWI	FRVLYRYPYQIIFGQIPLDEIDA	929
Db	198	MKDVFVFFFLCWMLVAVGAVTEGILRPQDRSLPSILRRVFRYPYQIIFGQIPQEBMDVA	257	
Qy	930	RV---NCS-----	THPLLEDSP---SCPSLYANWLVLILLVTFLLVTNVLNMLLIAM	977
Db	258	LMIPGNCMSMERGSHWAP---	EGPVAGSCVQYANWLVLILLVFLVANILLNLLLIAM	313
Qy	978	FSYTFQVQGNADMFWKFORNLYVEYHERPALAP	PPIILLSHLSLTLR-----RVFK	1029
Db	314	FSYTFKVNHSNLYWKAQYSLIRFHSRPAAPPLIIISHVRLIKWLRCRCRRAN	373	
Qy	1030	KEAHEKREHLERLDPDLPDQKVVTWETQKENFLSKMEKRRDSEGEVLKTAHRVDFTA	1089	

Db 374 LPASPVEPRVCLSKAEARKLLTWSVHKENFLLAQAQRKDSRSLKRTSQKVDLAL 433
 Qy 1090 KYLGRLREKRIKICLESQINYSVLVSVADVLAQGGPRSSQHCGBGSQSLVAADHGG 1149
 Db 434 KQLGQIREYDRRLRGLEREYQHCRLVTWAEALSH-----SALL----- 473
 Qy 1150 LDGWEQAGAGQPPSDT 1165
 Db 474 -----PPGAPPPPSPT 484
 RESULT 2
 T23707
 hypothetical protein T01H8.5 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T23707; T24342
 R;Kerhaw, J.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19786
 A;Accession: T23707
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1868 <WIL>
 A;Cross-references: EMBL:Z83117; PIDN:CAB05572.1; GSPDB:GN00019; CESP:T01H8.5
 A;Experimental source: clone M04C7
 R;Lennard, N.
 submitted to the EMBL Data Library, September 1996
 A;Reference number: Z19877
 A;Accession: T24342
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1868 <WIL>
 A;Cross-references: EMBL:Z80219; PIDN:CAB02303.1; GSPDB:GN00019; CESP:T01H8.5
 A;Experimental source: clone T01H8
 C;Genetics:
 A;Gene: CESP:T01H8.5
 A;Map position: 1
 A;Introns: 24/3; 112/3; 191/3; 220/1; 268/2; 375/2; 456/2; 552/3; 625/2; 744/3; 850/2; 1

Query Match 17.6%; Score 1070.5; DB 2; Length 1868;
 Best Local Similarity 24.5%; Pred. No. 5.7e-69;
 Matches 343; Conservative 231; Mismatches 486; Indels 341; Gaps 41;
 Qy 26 GEVNF-GSGKKRGKRVVPSPVAPSVLFDLLASWHLPAENLVSLVGBEQPFAMKSL 84
 Db 214 QGVFQGGPHPYKAYVRVNFTEPAYTMSLFHVWQISPRLLITVHGTSNFDLQPKL 273
 Qy 85 RDLRKGLVKAQSTGAWILTSALRVGLARHVQAVRDHSLASTSTKRVVAVGMSLGR 144
 Db 274 ARVFRKGLLKAATTTGAWIITSGCDTGVVGVAAALEG---AQSAQRNKVICIGIAPWG- 329
 Qy 145 VLHRRILREAEQDF-----PVHYEDDGGQGPLCLSDNSLSHFILVPPGPKGDLT 198
 Db 330 -----LUKKREDFIGQDKTVPIYP---SSSKGRFTGLNNRHSYFLLVNDGTVGRYGAEV 380
 Qy 199 ELRLREKHISQRAYGSGTSEIPVLCLVNGDPNLTLEISRAVEQA---APMLILVGS 256
 Db 381 ILRKELEWYISQKQIFGTHS--VPVVCVLEGGSCITIRSDYVTVNVRPVVVCDS 438
 Qy 257 GGIADVLAAL---VNQPHLL-----VPKVAEQKPKFKPSKHSFWMEDIVRWTKLLQNI 306
 Db 439 GRAADLAFAHQNVTEDEGLLPDIRRQVLLLVETTFGCEAAAH-----RLHHEL 488
 Qy 307 T---SHOHLTVYDEQSGSELDPTVILKALVKACKSHSQBPQDYLDELKLAWMDRVDI 363
 Db 489 TVCAQKNLLIFRLGEGEHVDVHAILTALKG-----QNLAAQDLALAAWNRVDI 542
 Qy 364 AKSEIFNGDVWKSCDLEEVMDVLVGNKPEFVRLFVDNGADVADFLTYGRLOELY---- 419
 Db 543 ARSDVFAMGHEWPPQAAALHANMAEALIHDRVDFVRLLEQGINMQKFLTISRLEDELNTDK 602
 Qy 420 -----RSVSRK-----SLLFDLL-----QRKQEEARL- 441

Db 603 GPPNTLFYIVRDVVRVQGYRFLKPLDGLVIEKLMGNSYQCSYTTSEFRDKQKMRKV 662
 Qy 442 -----TLAGLGTQARE-----PPAGPPA-F 461
 Db 663 HAQKAMGVFSSRSRTSGTSGIASRQSTEGMGVGGSSVAGVFGNSFGNQDPPDHPVNR 722
 Qy 462 SLHVSRLVKDFL--QDACRGFYODGRPGDRRAEKGPAKRPQTQKWLILLNOKSEN--- 516
 Db 723 SALSGSRALSNIHLWRSFRGNF---PANPMRPNLGDSDRDCGSEBDELSLTSADGS 778
 Qy 517 -----PWEDLFLWAVLQNRHEMATYFWAMQGEVAAALAAACKILKENS-----HLE 562
 Db 779 QTEPDFRYPYSELMIWAVLTKQDMAMCMQWQHEEAMAKALVACRLYKSLATAEADEYLE 838
 Qy 563 TEAABARATREKRYERLALDLFSECYSNSBARAFALLVRRNRQWSKVTCTLHLATEADA 622
 Db 839 VEICEELKYAEPRILLSLELDHCHYHDDAQTLLTYELSNWSNETCLALAVVNNKH 898
 Qy 623 FFAHDGVQAFTRIWMGDMAGT--PILRLLAGFLCPALV----- 660
 Db 899 FLAHPCCQILLADLWHGGLRMRTHSNIKVVVLGLICPPFIQMLEFKTREELNQPTAAEH 958
 Qy 661 -----YTNLITFGEAPLRTGLEDLQDLSLDE----- 689
 Db 959 QNDMNTSS 1018
 Qy 690 ----- 699
 Db 1019 LFHSRRRKAKNEKCDRETDAACEAGNRQIQNGGLTAEGTFTGESNGVSPPPPYMRANS 1078
 Qy 690 -----KSPLYGLQSRVEELVEAPRAQGR-----GPRAVFLTRWRKFW 728
 Db 1079 RSRYNNSDMKSTSSVIFGSDPNLSKLOKSNITSDRPNPMEQFOGTRKIKMRRRYEYF 1138
 Qy 729 GAPVTVFLGNVMYFAFLFTVTVLVDPRPPQGPSGPREVTLYFWFTLTVLEIRQGF 788
 Db 1139 SAPISFWSWTISFILFIPTTLLV--KTPPR-PTVIEYILIAVAAFGLSQVRKIM 1195
 Qy 789 TDETHLVKFTLYVGNWNKMDMVAIFLIVGVTCRMLPSAFEAGRTVLAMDPMVFTLR 848
 Db 1196 SDAPK-PYEKIRTYVCSFNCVTLAIIFIVGFFMRCFSGV-AYGRVILACDSVLWTMK 1253
 Qy 849 LIHIFALHKQLGPKLIIVEREMKDVFFLFFLSVMLVAVGTVTQALLHPHDGRLEWIF-R 907
 Db 1254 LLDYMSVHPKLGYPVTMAGKMIQNMSYIIVMLVTLLSFLGARQSITYP-DETMHWILVR 1312
 Qy 908 RVLRYRPLQIFGQIPLDEIDEARVNGSTH-----PLLEDSP---SCPSLYANWL 954
 Db 1313 NIFLKPYFMYLGEVYADEID---TCGDEADQDHLNGGPFVILNGTTGLSCVPGY--WI 1366
 Qy 955 VILLVTFLLVTVNVLNMLLIAMFSYTFQVQGNADMFWKFORYNLIVRYHERPALAPPF 1014
 Db 1367 PPLMTFFLLIANILLMSMLIAIFNHIFDQTDMSQOIWLFQRYKQVMEYESTPFLPPL 1426
 Qy 1015 ILLSHLSLTIRRVFKKEAEKHSEH-----LEEDLPDLDQKVVTWETQKENFL-S 1064
 Db 1427 TPLYHGVLILQFVTRLSCKSQERNPILLLKIAELFDNDQIEKLHDFEEDCMEDLARQ 1486
 Qy 1065 KMEKRRDSEGEVIRKTAHR-----VDFIARYLGG---LREQEKRIKCLSSQINCSV 1114
 Db 1487 KMEKTSNEQIRLADIRTDQILNRLIDLQAKESMGROVDINDVESRLASVEKAQN---E 1543
 Qy 1115 LVSSVADVLACGGPRSSQHC 1135
 Db 1544 ILECVRALLQNNAPTAIGRC 1564

RESULT 3

T22644

hypothetical protein F54D1.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T22644
R;Lennard, N.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19592
A;Accession: T22644
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1400 *WIL>
A;Cross-references: UNIPROT:Q20766; EMBL:Z77132; PIDN: CAB00861.1; GSPDB:GN00022; CESP:FS
A;Experimental source: clone F54D1
C;Genetics:
A;Gene: CRSP:F54D1.5
A;Map position: 4
A;Introns: 21/2; 51/2; 205/2; 276/3; 364/2; 394/2; 466/3; 507/3; 536/3; 599/3; 672/2; 692/2

	Query Match	16.4%; Score 1000; DB 2; Length 1400;
	Best Local Similarity	27.8%; Pred. No. 5e-64;
	Matches	335; Conservative 204; Mismatches 478; Indels 188; Gaps 46;
Qy	26	GEVNF--CGSGKGRKGFVRVPSGVAPSVLFOLLIAEWHLPAPNLVSVLVSQEPQPAKMSWL 84
Db	151	GTIVFGGAHAHKAQYVRLSYDSPLDMVYLMKVGLEAPRLVITVHGMSNFELEERL 210
Qy	85	RDVLRKGLVKAQSTGAWILTSALRGLARHVGQAVPDHSLASTSTKRVVAVGMSLGR 144
Db	211	GRLPFRKMLKAAQQTGAWITSGLDGSGVVRHAKAL--DEAGISARMSQIVTIGIAPWG 269
Qy	145	VLRHRIIEEAQEDPPVHYPEDDGGSGPLCSLNSLSHFILVBPFGPKGDLTELRRL 204
Db	270	IKRKERLIRQNEH--VYDVHLSVNAVGLINDRHSYFLLADNGTVGRFGADLHLRQNL 327
Qy	205	EKHISEORAGYGGTGSIEIPVLCILLVNDPNTLERISRAV--EQAPWLILVSGGGIADV 262
Db	328	ENHI-----ATFGNGR--KVPVCTLLEGGISSIAIHDIYVTMKPDIPIAIVCDGSGRAADI 382
Qy	263	L---AALVNPQLLVKVAEK---QFKEKPSKHSFHWEDIVRTKLLONITSHOHLITVY 316
Db	383	ISFAARYNSDGTFAAEVGEKRLNLIKWFPET--DOSEMPR--KITECVI-RDILLRIIF 437
Qy	317	DFEOGSEELDTVILKALKACKSHSQBPQDLDLDELAVAWDRVDIAKSEIFNGDVEWK 376
Db	438	RYGEEBEDVDVILSTVLQ---KQNLPPD--EQLALTSWNVRVDIAKCLFSNGRKN 491
Qy	377	SCDLEEVMDVALSNKPFVRLFDVNDGADVADFLTYGRLOLY-----RSYRSKSL 428
Db	492	SDVLEKAMDALYWRDVFVCELEENGVSVMKNFLSINRLNLYNWDINDSAHSVRNWMEN 551
Qy	429	FDLIQRKQSEARLTLAGLGTQOAREPPAPGAPAPSLHSEVSRVLKDFLQDACRGFTQDRPG 488
Db	552	FDSM---DPHTYLTIPMIG--QVVEKLMG-NAFQLYYTSRSFK-----GKYD 592
Qy	489	DRRAEKCP---AKRPTGOKLL-----DLNQSEN-----PWRDLFLWAVLQNRHEM 533
Db	593	RYKRINQSSYFHRKRRKIVQKELFKKSDQDINDNEEDFSFAYPFNDLLIWAUITSRHGM 652
Qy	534	ATYFWAMQEGVAALAAACKILK-----EMSHLETEAARATREA--KYERLALDLFSE 586
Db	653	AECMVVHGEDAWAKCLLAILYKATAKTAIEYLDVE-EAKRLPDNAVCKREDALIELDQ 711
Qy	587	CYSNSEARAPALLVRRNRCWSTTKCHLATEADAKAPFAHDGVQAFLTRIWWGDM--NAG 644
Db	712	CYRADHRTLRLLRMELPHWGNNGNCLSLAVLANTKTFLAHPCCQILLAEHLHGSLKVRSG 771
Qy	645	TPILRLGNFLC-PALVY-----TNLIITFSEAPLRTGLEDI-QDLDSLDTEKSPLY 694
Db	772	SNV-RVLTAICPPAILFMAYKPKHSKTARLLSEETP-----EQLPYPRESITSTSNRY 825
Qy	695	GLQSRVEELVEAPRAQG-----DRGPRAVF-----LITRWK 726
Db	826	RYSKGPEQKETLLEKGSYTKVTIISRKSGVASVYGSASSMMFKREPQLNKFEPRA 885
Qy	727	FWGAPVTYVFLGNVVMYFAPLFTYVLLVDFFRPPQPGSGPEVTLYFWVFTLVLEETRQ 786

Db 426 APAHQVQSQFSLSDNRNQLNVRIRFYGYDPKTAQKLKIQ----- 467
QY 303 LQWITSHQHLTVYDFEQSGSELDVTILKALVACKSHSQBPQDYLDLKLAVAMDVRD 362
Db 468 IVECSSTNKLMTIFRLGSSREDLHVIMSCLL---KQNLSP---EQQLALANRAD 521
QY 363 IAKSEIFNGDVWKSCLDEEVMVDALVSNKPEFVFLFVDNGADVADFLTYGRLOELY--- 419
Db 522 IARTIFANGTEWTTQDLNAMIETALSNDRIDFVHLLLENGVSMQKFLTYGRLEHLNNTD 581
QY 420 ---RVSRSKSLFDLLQKQBEARLTLAGLTQQAEPAPPAFAFHSVRSVLKDFLOD 476
Db 582 KGQONTLRNLVDSKHH-----IKUVEGRVLNVLNMG 615
QY 477 ACRGPFYQD-----GRPDERRAEK----- 495
Db 616 LYKSNYTKBEFNQYFLFNNRKQFGKRVHNSNGRNDVIGPSGDAGRSMMSQJSLIN 675
QY 496 -----GPAKRTGQKWLDLNOKSEN-----PWRLFLWVLQNHWMATY 536
Db 676 NARNSIISLFGCGGKRESDEDDFSLNEEANNWDTFRYPYSDLMWVLTTRKQAKL 735
QY 537 FWAMQGEVAAALACKILKEMSHLFEAEARATREA-----KYERLALDLFS 585
Db 736 MWTIGBEGMAKALVASRL-----YVSLAKTASLTGEMSGQDFTBFSDEFSSELAVEVLE 790
QY 586 EYGSNSERAPALLVRNRCWSKTTCLHLATEADAKAFPAHDGVOAFLTRIWWGDMA--- 642
Db 791 YCTKHGRDQTLRLTLCELANWGETCLSLAANGHRRKFLAHPCQMLSLDQGLLMKN 850
QY 643 -AGTPILRLLAGFLCPALVTNLIITSEAPLR-----TG 676
Db 851 NQNSKVLTCIAA---PPLIF--LLGFRTKEQLMLQPKTAAHDEEMSDSEMSAEDTDS 905
QY 677 LEDQLDLSLDT-----KSPLYGLQSRVEELVEA 706
Db 906 SDSSDDSDDEDAKLRAQSLADQPLSIHLRLVRDKLNFSEKKPKDMG---ISRIVVA 961
QY 707 P-----RAQ----- 710
Db 962 PPIVTRGNRARTMSIKKSKNVIKPPACLKIETSDDEQEKATCKMCKSTFFDFPDP 1021
QY 711 ---GDRGPRAV-----FLTR-----WRK 726
Db 1022 YINRTGKGSVAMNHDMDYDPSBELDTQTRQKSSREFSSRNVTYQVTRPLSMKK 1081
QY 727 ---FWGAPVTVLGNVMYFA---FLFLTYYLLVDFRPPPPQSGPGEVTLXFWVTLV 779
Db 1082 KIMEFYKAPITTYW---LWFFAFIWFLLITLNLVKTQ---RTASWSEWVYFAYIFWT 1135
QY 780 LE---BIRQGFTEDETHLVKFKTLVVGDNWKNCDMAIFLIVGVTCRMLPSAFAEAGRT 836
Db 1136 LEIGRKVSTIMMDTSKPVKQLRVFFQYRNGLLAFGLLTLYLAYFIRLSPTTKTLGRI 1195
QY 837 VLAMDPMVFTLIIHFAIHKQLGPKIIVVERMKNDVFFFLFSLVMAVGVVTTQALLH 896
Db 1196 LIICNSVMSLVDLSVQOGLGPIYINVAEMIPMLPLCVLVFTLYAFGLRQSTY 1255
QY 897 PHDGRLEW---IFRRVLVRYLQIFGQPLDEIDBARVNCSTHPLLEDSPSCPSLYAN- 952
Db 1256 PVE---DHWHLVRNIFQTFMYLGEVYAAEID---TCGDEIWTQTHEDENIPISMLNV 1308
QY 953 ---WLVLVLLVTLVTLNVLNMLLIAMFSYTFQV-VQGNADMWKEQRVNLIV 1002
Db 1309 THETCVPGYWTAPVGLTVFMLATNVLNVMVWVAGCTVIFEKHQSTREIF-LFERVQGMV 1367
QY 1003 EYHERPALAPFILLSHLSLTLRVFKKEAHEHLEH-ERDL-----PDLQKQVWTET 1056
Db 1368 EYESTWLPPTFTIYHVIMFKLIKSSSRMRERKNLFDQSLKFLSPDEM-EKVHTPEE 1426
QY 1057 VOKENFLSKMEKRDRDSEGEVLRKTAHRVDVFIKYLGLL-----RQEKRIKCL 1105

Db 1427 ESVDKRETEKNLSSNDRIRHTAERTDAILNRVSHLTQLEFTLKEIRELSHKMKQM 1486
QY 1106 ESQ 1108
Db 1487 DSR 1489

RESULT 5
JU0092
trp protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-Nov-2000
C:Accession: JU0092
R:Montell, C.; Rubin, G.M.
Neuron 2, 1313-1323, 1989
A:Title: Molecular characterization of the Drosophila trp locus: a putative integral mem
A:Reference number: JU0092; MUID:90180449; PMID:2516726
A:Accession: JU0092
A:Molecule type: mRNA
A:Residues: 1-1275 <MON>
A:Experimental source: strain Oregon R
C:Comment: trp protein is expressed predominantly in the rhabdomeric membranes of the ph
C:Genetics:
A:Gene: trp
A:Cross-references: FlyBase:FBgn0003861
C:Superfamily: TRPC3 protein
C:Keywords: transmembrane protein
F:334-354/Domain: transmembrane #status predicted <TM1>
F:378-401/Domain: transmembrane #status predicted <TM2>
F:419-436/Domain: transmembrane #status predicted <TM3>
F:457-471/Domain: transmembrane #status predicted <TM4>
F:504-527/Domain: transmembrane #status predicted <TM5>
F:612-630/Domain: transmembrane #status predicted <TM6>
F:636-661/Domain: transmembrane #status predicted <TM7>

Query Match 5.4%; Score 326.5; DB 2; Length 1275;
Best Local Similarity 20.3%; Pred. No. 4.8e-15;
Matches 178; Conservative 123; Mismatches 264; Indels 313; Gaps 37;
QY 305 NITSHQHLTVYDFEQSGSELDVTILKALVACKSHSQBPQDYLDLKLAVAMDVRDIA 364
Db 86 NVILLHEHTEVGDALLHAISEEYVEAVEEQLQWETNKEGQPY-----SWEAVDRS 137
QY 365 KSEIFNGDVWKSCLDEEVMVDALVSNKPEFVRLFVDNGA-----DV 406
Db 138 KS-TFTVDI-----TFLIAHRNNYELIKILLDRGATLPMPHDVKCGCDECVTSQT 188
QY 407 ADPLTYGRILQ-ELYRSVRSKSLIPDLLQKQBEARLTLAGLTQQAEPAPPAFAFSLH- 464
Db 189 TDSLRSQSQRINAYBALSSLI-----ALSSRDPLV--TAFQLSW 227
QY 465 EYSRVLKDFLODACKGFGVQDGRPGDGRRAEKPAKRPRTGQKWLDLNOKSENPMRDILFW 524
Db 228 ELKRL--QAMESFEAEYTEM--QMVDPGTS-----LLDHARTS-----MELE 268
QY 525 AVLQNRHEMATYFWAMGOEGVAAALAAACKILKEMSHLFEAEARATREAKYERLALDLP 584
Db 269 VMLNPNHPSHDINCLGQ-----RQTLER----- 292
QY 585 SECYNSERAPALLVRNRCWSKTTCLHLATEADAKAFPAHDGVOAFLTRIWWGDMAAG 644
Db 293 -----LKLAIYKQKTFVAHPNVQQLAAIIVD---G 321
QY 645 TPILRLLAGFLCPALVTNLIITSEAEPLATGLDEDLQDLSLDTKSPLYGLQSRVEELV 704
Db 322 LPGRF-----RQASQQLMDVVKGC-SFFIYSL-----KYI 352
QY 705 EAPRAQDGRGPRAVFLITRWRKFWGAPVTVFLGNVVMYFAFLF----- 748
Db 353 LAPDSEG-----AKENRKPFFKFIHSCSYMFFFLMLLGAASLRVVVQITFELL 399
QY 749 -FTYVL--LVDFRPPPGQ--PSGPEVTLVFWVTLVLEIR-----QGFTDETHLVKKF 799

Db 400 APPMWTLEDRKHERGSLPGPIELAITIYIMALIFEELKSLYSDGLFE----- 449
Qy 800 TLYVGDWVWVCDMAIFIVGVTCR-----MLPS 829
Db 450 --YIMDLNWIIVDYISNMFYVWILCRATWVWVHRDLWFRGIDPYFPRHHHPDPDMLLS 507
Qy 830 --APEAGRTVLAMDPMVFT-LRLIHFIAHFKQLGPKIIVVERMMKDVFFFLFSLVWLVA 886
Db 508 EGAFAG-----MVFSYKLWIFSIINPHGLPQVSLGRMIIDIIKFFFIYTLVLF 559
Qy 887 YGVTTQALL-----HPHGRLEW-----IFRRV--LYRP-----YLOIFGQ 920
Db 560 FCGGLNQLLWYVAELEKNCVHLHPDVADFDQEKACTIWRFSNLFETQSQSLFWSFGL 619
Qy 921 IPLDEIDARVNCSTHPLLEDSPSCPSLYANWLIVLLVTFLLVTVNLLMNLIAFESY 980
Db 620 VDLVSFIDLAKIS-----FTRFWALLMFSGYSYVINIIVLLNMLIAMNSN 663
Qy 981 TFOVVGQADMFVFORNYNLIVEYHE-RPALAPPFILLSHLSLTLLRRVFKKEAEHREHL 1039
Db 664 SYQIIISERADTEWKFARSOLMWSYFEDGGTIPPPNLCPNMKMLKTLGRKPSRTKSM 723
Qy 1040 ERDL--PDPLQDVVTVQKCNFLSKMEKRRDSEG 1075
Db 724 RKSMEQAOTLHDKVM---KLLVRYIT-AEQRRDDYG 757

RESULT 6
JN0015
trp protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001
C:Accession: JN0015
R:Wong, F.; Schaefer, B.L.; Roop, B.C.; LaMendola, J.N.; Johnson-Seaton, D.; Shao, D.
Neuron 3, 81-94, 1989
A:Title: Proper function of the Drosophila trp gene product during pupal development is
A:Reference number: JN0015; PMID:2482778
A:Accession: JN0015
A:Molecule type: mRNA
A:Residues: 1-1274 <WON>
C:Comment: This photoreceptor membrane-associated protein is not required for the occur
C:Genetics:
A:Gene: trp
A:Cross-references: FlyBase:FBgn0003861
A:Map position: 99C5-6
C:Superfamily: TRPC3 protein
C:Keywords: glycoprotein; nucleotide binding; P-loop; phosphoprotein; transmembrane pro
F:1257-1263/Region: nucleotide-binding motif A (P-loop)
F:64,70,899/Binding site: carboxylate (Asn) (covalent) #status predicted
F:191,602,880,883,924/Binding site: phosphate (Ser) (covalent) #status predicted
F:800,1266/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 5.2%; Score 317.5; DB 2; Length 1274;
Best Local Similarity 20.3%; Pred. No. 2.2e-14;
Matches 187; Conservative 132; Mismatches 273; Indels 327; Gaps 41;

Qy 274 VPKVAK-QPEKFPKSHSWEDIVRWTKLLQNTSH-----QHLLTVDFDQEGS 323
Db 48 VKKILEYQGTDFK---NINCTDPMNRSALISAENENFDMLVILLIEVGDALLHAI 104
Qy 324 BELDTVLKALVACKSHSQEPQDYLDELKLVADWRVDIAKSEIFNGVEMKSCDLEEV 383
Db 105 SEBYEVAEVELLQWEETHNHEGQPY-----SWEADVRSKS-TFTVDITF----- 147
Qy 384 MVDALVSNKEFVRLFDNGA-----DVADELTVGRILQ-BLYRSVSR 424
Db 148 LILAAHNNYIILKILLDRGATLPMPHDVKCGDCQVTSQTSLRHSQSRINAYALSA 207
Qy 425 KSLFLDLLQKQBEARLTLAGLQQAQREPPAGPAPSLH-EVSRVLKDFLQDQACRGFYQ 483
Db 208 SSLI-----ALSRDPVL--TAPQLSWELKRL--QAMESEFAEY 244
Qy 484 DGRPGDRRAEKGPAPKPTQCKQLLDLNQKSENPWRDLFLWAVLQNRHENATYFWAQGE 543

Db 245 EMR---QWVODFGTS-----LLDHARTS-----MELEVMLNFNHPSHDIW----- 282
Qy 544 GVAALAAACKILKEMSHLETEAEARATREAKYERLALDLFSECVSYSEARAFALLVVRN 603
Db 283 -----CLASSET-----LER-- 292
Qy 604 RWSKTTCLHLATRADAKAFPAHDGVQAFALFRIWGDMAAGTPILRLGLGAFCLPALVTN 663
Db 293 -----LKLAIRYKQKTFVAHPNVQQLAAIW-----YDG 321
Qy 664 LITSEERAPLTGLDLODSLDEKSPLYGLQSRVEELVEAPRAQDGRGRAVFLLTR 723
Db 322 LPPGPOEAS-----QQLMDVVVKLGC-SPIIYSL-----KYLAPUSEG----- 358
Qy 724 WRKKGWAPVTVFLGNVVMYFAPLFL-----FTYVL--LVDFRPPQO-- 763
Db 359 -AKWRNPLSSSRTPCPSYMFLLMGLGASLRVQVITFELLAFPMWLTLEDWRKHERGS 417
Qy 764 -PSGPEVTLYFWFTVLEER-----QGFTEDETHLVKFTLYVGDNNKCDMAIFLF 818
Db 418 LPPGIELAITIYIMALIFEELKSLYSDGLFE-----YIMDLNWIIVDYISNMFY 465
Qy 819 IVGVTCR-----MLPS--APEAGRTVLAMDPMVPT 846
Db 466 VTWILCRATAWVIVHRDLWFRGIDPYFPRHHHPDPMLLSEGAFAG-----MVFS 517
Qy 847 -LRLIHIFAIHKQLGPKIIVVERMMKDVFFFLFSLVWLVAYGVTTQALL----- 895
Db 518 YLKLWHIFSIINPHGLPQVSLGRMIIDIIKFFFIYTLVLFAGCGLNQLLWYVALEKMK 577
Qy 896 --HPHGRLEW-----IFRRV--LYRP-----YLOIFGQIPLDEIDARVNCSTHPL 939
Db 578 CYHLHPDVADFDQEKACTIWRFSNLFETQSQSLFWSFGLVDFVSLDLAGIKS----- 631
Qy 940 LEDSPCSPLSYANWLIVLLVTVNLLMNLIAFESYTFVQVGNADMFVQRYN 999
Db 632 -----FTRFWALLMFSGYSYVINIIVLLNMLIAMNSYQIIISERADTEWKFARSQ 681
Qy 1000 LIVEYHE-RPALAPPFILLSHLSLTLLRRVFKKEAEHREHLERDL--PDPLQDVVTVTWT 1056
Db 682 LMWSYFEDGGTIPPPNLCPNMKMLKTLGRKPSRTKSFMRKSMERAQTLHDKVM--K 738
Qy 1057 VOKENFLSKMEKRRDSEG 1075
Db 739 LLVRYIT-AEQRRDDYG 756

RESULT 7
S40764
hypothetical protein ZK512.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: S40764
R:Hawkins, T.; Ainscough, R.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40759
A:Accession: S40764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1418 <HAW>
A:Cross-references: UNIPROT:P34641; EMBL:Z22177; NID:g297989; PID:g297992
C:Genetics: 199/1, 238/1, 290/2, 529/3, 557/3, 588/3, 677/2, 733/3, 772/3, 846/3, 946/1;
A:introns: 199/1, 238/1, 290/2, 529/3, 557/3, 588/3, 677/2, 733/3, 772/3, 846/3, 946/1;
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK512.3

Query Match 4.8%; Score 294; DB 2; Length 1418;
Best Local Similarity 20.2%; Pred. No. 1.3e-12;
Matches 222; Conservative 174; Mismatches 437; Indels 264; Gaps 45;

Qy 65 PNLVSLVGEQEPFANKSWLRDLVRLKGLVKAQSTGAWILTSALRVGLARHVQAVRDHS 124
Db 67 POLIISLISHGNSLSTK--YMSSVENGLKSLFGCGTWLISSG-----EYNDPM 113

Db 430 LELIVVMYVIGFVWEVEQEIFAVGMSK-----YLRNMWNFIDFLRNSLY-VSVMC-L 479
Qy 827 LPSAFAGRTVLAMD-----FMVET-LRLIHFIAHKQL 859
Db 480 RAFAYIQOATARDPQOMAYIPREKWHDFDPQIAEGLFAAANVPSALKVHLFSINPHL 539
Qy 860 GPKIIVVERMMKDV--FFFLPFLSVMLVAYGVTT-----TQALLHHDGRLEW-- 904
Db 540 GPLQISLGRWIDIVKFPFIYTLVLFAPACGLNQLLWTFYFALEKSKCVLP-GGEADWGS 598
Qy 905 -----IPRRV--LVRP-----YLQIFQIPIDEIDARVNCSTHPLLEDSPSCPSLYAN 952
Db 599 HGDSCKWRRFGLNLFESSQSFLWASFGVMGLDDFELSGIKS-----YTR 642
Qy 953 WLVLILLVTFLLVTVNLLVLLIAMSFTYFQVQGNADMFVKFQRYNLIVYHERPA-LA 1011
Db 643 FWGLMFGSYGVINVLNLLIAMSYSYAMIDSHSTEWKFPATKLWMSYFEDSATLP 702
Qy 1012 PPFILLSHLSLTLRRVFKAEHREHLERDLPDQKVVTVQKENVFSLKMKERRR 1071
Db 703 PPFNVLPVKVI-RIFKSS-----KTIQRQSKRKEQOF 739
Qy 1072 DSEGEVLKTAHRVDVFIKYLGLREQ-----EKRIKLESQIN 1110
Db 740 SEYDNIMR-----SLVRYVAAMHRKPNPNVSEDDINEVKSEIN 779

RESULT 9
F88391
protein R06B10.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: F88391
R:Anonymous, The C. elegans Sequencing Consortium.
S:Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; PMID:99069613; PMID:9851916
A:Note: see website genome.wustli.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: F88391
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-899 <STO>
A:Cross-references: GB:chr_III; PIDN:AA895033.1; PID:g2746879; GSPDB:GN00021; CESP:R06B1
C:Genetics:
A:Gene: R06B10.4
A:Map position: 3

Query Match 4.1%; Score 247; DB 2; Length 899;
Best Local Similarity 19.4%; Pred. No. 1.7e-09;
Matches 166; Conservative 125; Mismatches 312; Indels 252; Gaps 38;

Qy 349 LDELKLAVDNRVDIAKSEIFNGDVEWKSDDL-----EYVMDALVSNKPEFVRLFDV 401
Db 32 LREKQPLLSCERCDIGSVRKLAGISTEFTNCLDPLGRNALLIAENIEMIELLD 91
Qy 402 NGADVADFTYGRQELYSVSKSLFLDLQKQBE-EARLTLAGTQOQAPPPAGPPA 460
Db 92 HNITGDAILYAIGEE--NVEAVEIIVHELEKMDKFDSEKQGVETESAFPTDITP 148
Qy 461 FSLHEVSRVLKDFLODACHGFFYODGRPDERRAEKPAKRP-----TGQKWL 508
Db 149 LAAH-----KONYE--CIKFLD-----KGTVPHPHDVRCSPCEYVARBEDSL 191
Qy 509 DLNOKSENPRDLFLWAVL--ONRHEMATYFWAQGVAAALAAACKILKEMSHLETAEBA 567
Db 192 RLRSRINAVRALTSPSLICLSARDPILYAFELSW-----LKELSFIEFPRT 240
Qy 568 ARATREAKYERLALDFSECYSNSEARAFALLVRNRCWKTTC-----LHAT 616
Db 241 DYEELSQKQKFCVHMLDQVRGSKLE--VVLNHTTNAMHDVTSANYGNPEKLARKLAI 298
Qy 617 EADAKAFFAGHDGVOAFLTRIIWGDMAAGTPIRLGLNGLCPALVYTNLITFSEAPLRTG 676

Db 299 QLSQKRFVAHPNCQQLLDIWIY-----EGVESVR-----CTNFIY-KLIFY----- 338
Qy 677 LEDQLDLSLDTEKSPLYGLQSRVEELVEAPRAQGRGPRAVFLL-----TRWRKFWGADVT 733
Db 339 -----ILGMLGFLPFLSL-----VYLLAPHSSMGQFAKKPFI 369
Qy 734 VFLGNVVMYFAFLFITY-----VLIVD-----FRPPQGSPPGVETLYFWVFT 777
Db 370 KFLSHSGSYIFFILLIMASQRMVNIDILRTDDVDKRETRGPP--PTIIECAIFLWVLG 427
Qy 778 LVLEBIRQ-----GFTTBEDTHLVKFTLYVGDNNKCDMVAIFLFIIVGTCTBML----- 827
Db 428 LIWVEIKQLWECGLYN-----YCRNLWNILDFITNSLYLTALRVVAIVQVE 475
Qy 828 PSFAEAGR-----TVLAMDFM-----VF-LRLIHFIAHKQLGP-KII 864
Db 476 QEALRANSVHTARHLPRRDWDAMPDLLSECFPATANIFSSLKLVHITVSPHLGPKLIS 535
Qy 865 VVE-----RMMKDV--PFFFLSVMLVAYGVTTQALLPHDGRLEWIFRRV- 909
Db 536 LGELEKFWKKTLCRMVIDIVKFFMVYALVLFACGL-----NOLLWYASMR 585
Qy 910 -----LYRPY-----LQIFGQIPIDEIDARVNC-----THPLL 940
Db 586 QNECNLYEQYKNEKSLSYKYEHLKESCDKCYKSCSIYHTAETLFWALFGLVDLTHFLK 645
Qy 941 EDSPCPSLYANLWILLVTLVTVNLLIAMSFTYFQVQGNADMFVKFQRYNL 1000
Db 646 ED-----HFLSEWGTGKTIFGYSYCCSIIVLNLMIAMNSYQYISDQADIEWKARSRL 700
Qy 1001 IVEYHERPA-LAPPPILL-----SHLSLTLRRVFKAEHREHLERDLPDQKVVTVWET 1056
Db 701 FLEYFDDTATLPPPNIVPSKSIYYLHLYTLKLCNCTK-----LQOPSKOKSM--R 751
Qy 1057 VOKENFLSKMEKRRR 1071
Db 752 VESKNLAIRQRPKQ 766

RESULT 10
S44873
ZC21.2 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C:Accession: S44873
R:Du, Z.; Waterston, R.
S:submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZC21.
A:Reference number: S44649
A:Accession: S44873
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-823 <DUZ>
A:Cross-references: EMBL:L16685; NID:g289729; PIDN:AAA28168.1; PID:g289732
C:Genetics:
A:Introns: 47/2; 91/3; 144/1; 215/2; 344/3; 394/3; 440/3; 506/2; 566/3; 756/3
C:Superfamily: TRP3 protein
C:Keywords: transmembrane protein

Query Match 3.9%; Score 235.5; DB 2; Length 823;
Best Local Similarity 20.7%; Pred. No. 1e-08;
Matches 113; Conservative 92; Mismatches 190; Indels 151; Gaps 20;

Qy 549 LAACKILKEMSHLETAEAAAT---REAKYERLALDFSECYSNSEARAFALLVRNR- 604
Db 260 LSAFLKSWDLQRLAFEEHFKETYLQSRQCKYQSCDLLSQCRSEE--VIAILNKDGNV 317
Qy 605 -----CWS---KTTCLHLATEADAKAFYAHGVOAFLTRIIWGDMAAGTPIRLGLA-- 653
Db 318 NDDNIDVWASKLSLSRLKLAIKYEQKAFVSHPHCQQLTSITWY-----EGIPRQRSGTWA 373
Qy 654 --FLCPALVVTNLTITPSEAPLRTGLDQLDLSLDTSEKSPLYGL-----QSRVBEELVE 705

```

Db 374 NFELYAFLLF-----WPIFCLMYILMPKSLRGLR 405
QY 706 APRAQGRGPRVFLLRWRKFGAPVTVFLGNVVMYFAFLFETVLLVDP----- 757
Db 406 SP-----FMKPFYYSVS-----PATFGLLTWATFEDRYEKGEG 441
QY 758 ---RPPQPGSGP---EVTLYFWVFLVLEEIRQGFPTDTHLVKKFTLYVGDNNKCDM 812
Db 442 GMTRASDRPPATWVESLFTWVIGMLWSEIKQLW-----BEGFKRYMRQWNWLD 493
QY 813 VAIFLIVGTCRMLPSAFE-----AGRTVLAMDPMVTLR 848
Db 494 LMICLYLCTISRL--SAYIITYREDPYRTVRYTWTSEPMVLVASALFAGNVFSFAR 551
QY 849 LIHIFAIHKQLGPKLIIVVERMKOVFFFLFSLVNLVAYGVTTOALLPHDGRLEWIFRR 908
Db 552 IYLFQTNPYLGPLQISLGCMLVDVAKFCFIVLIISFSIGLAQLWYDPTDVCPLG 611
QY 909 VLYRPLYQIFGOIPLEIDEARVNCSTHPLLL-----EDSPSCPS-LYANWLVL 958
Db 612 ATCKHSSNVFSSI-----ADSVLTLLWSLFSITKPEDTDVVENHKITQWVGQGM 660
QY 959 LVTFLLVTVNLLMILLIAMPYTFQVQGNADMEWKFQRYNL-IVEYHERPALAPP-IL 1016
Db 661 FMVHCTSIIVLLANMLIAMMHSFQIINDHADLEWKFRTKLMAHFEDESSLPFPFNII 720
QY 1017 LSHLSL 1022
Db 721 VTPKSL 726

```

RESULT 11

JC5807
trp3 protein - rat

C/Species: Rattus norvegicus (Norway rat)
C/Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
C/Accession: JC5807
R/Preutz, K.D.; Noeller, J.K.; Krause, E.; Gobel, A.; Schulz, I.
Biochem. Biophys. Res. Commun. 240, 167-172, 1997
A/Title: Expression and characterization of a trp1 homolog from rat.
A/Reference number: JC5807; MUID:98042538; PMID:9367904
A/Accession: JC5807
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-828 <PRE>
A/Experimental source: brain
C/Comment: This protein participates in store-operated Ca2+ entry into cells.
C/Superfamily: TRPC3 protein

Query Match 3.2%; Score 192; DB 2; Length 828;
Best Local Similarity 19.8%; Pred. No. 1.5e-05;
Matches 154; Conservative 122; Mismatches 290; Indels 210; Gaps 31;

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QY 381 EEWVDALVSNKDFVRLFPVDN----GADVADFLTYGRQLYRSVRSKSL-LPDLLOK 435
Db 40 EERFLDAEYGNIPVVRKMLLESRTLVNVCVDMQNALQ---LAVGNEHLEVTEILLKK 96
QY 436 QBEARLTLAGL-----GTQOAREPPAGPAPSLHEVSRVLKDFLODACRGFYQGRPGDR 490
Db 97 ENLARIGDALLAISGVYRIVEAILSHPALAQOQTLSPLS-LRD--DDFYD----- 146
QY 491 RRAEGPKAKRPT-----GQKW-----LDDLKQSENPNRDLFLWVLQNRHEMAT-- 535
Db 147 ---EDGTRFSPDITPILAAHCHKYEVVHLLKGRTERPHDYLCRCADCAEQRUMTFS 203
QY 536 -----YFWMQEGVAAALAAACKILKEMSHLETEAEARATREAKYERLA 580
Db 204 HSRSRINAYKASPGYLSLSEDPVLTALELSNELAKLANIEKEFKNDYRKLMSQCKDFV 263
QY 581 LDLFSECVSNEARA-----FALLVRNRCSKTTCLHLATEADAKAFADHGVQAFLTR 635
Db 264 VGVLDLRCRDESEVAILNGDLESVEERHGHKASLSRVLKAIKYEKVFVAPNCQQLIT- 322

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QY 636 IWMGDMACTPILRLIGALFCLPALVYTNLITFSEAPLRTGLEDLQDLSLDTSKSPLYG 695
Db 323 IWGNLSGRGRIAIKCL-VVLVVALALPFLAIGYWIAPC----- 359
QY 696 LOSRVEELVEAPRAQGRGPRAVFLLRWRKFGAPVTVFLGNVVM---YFAFLFPTY 751
Db 360 ---SLGKILRSP-----FMKFAVASFIIFGLLVFNASDRFEGCITTLPN 401
QY 752 VLLVD-----FRPPQPGSGPEVTLYFWVFLVLEEIRQGFPTDTHLVKKFTLYVGDN 806
Db 402 ITVIDYPKQIRVKVTKTQFTWTEMLIMVVLGMWMECKELWLEGPREYIVQL----- 453
QY 807 NKKCDMAVFIPIVGVTCRML----- 827
Db 454 WNVLDPLSI--FIAAFARFLAFLAQTKAQYVDSHVQESDLEVTLPPEVQYTYARDKW 511
QY 828 ---PSAPEAGRTVLAMDPMVTLRLHIHFAIHQKLGPKLIIVVERMKOVF-PFLFPLSV 882
Db 512 LPSPDQIISGLYAIAYV-VLSFSRIAYILPANESFGPLQISLGRITVKDIFKPMWLFIW 569
QY 883 WL-----VAYGVTTOALLPHDGRLEWIFRRVLYRPLYQIFGOIPLEIDEARVNCST 935
Db 570 FLAFMIGHFILYSYLGAKVDPAFTTVESFKTLFW---SIFG---LSEV-----T 614
QY 936 HPLILEDSPSCPS-----LYANWLVLVLLVTFLLVTVNLLMILLIAMPYTFQVQGNADM 991
Db 615 SVVLKYDHKEFIENIGVLYGIYNTVMV-----VLLNMLIAMINSYQIEIDSDV 665
QY 992 FWKQRYNLIVEYHERPALAPPIL---LSHLSLTLRRV-FKKEAEHREHLERDL 1043
Db 666 EWKPARSKLWSYFDGDKTLPPPLVPCPSFYVFMRIVNPFK---CRRRLQKDI 718

```

RESULT 12

S68238
trp-1 protein - human

C/Species: Homo sapiens (man)
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S68238
R/Zhu, X.; Chu, P.B.; Peyton, M.; Birnbaumer, L.
FEBS Lett. 373, 193-198, 1995
A/Title: Molecular cloning of a widely expressed human homologue for the Drosophila trp
A/Reference number: S68238; MUID:96033971; PMID:7589464
A/Accession: S68238
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-793 <ZHU>
A/Cross-references: UNIPROT:P48995; EMBL:U01110; NID:g1072042; PIDN:AAA93251.1; PID:g107
C/Superfamily: TRPC3 protein
C/Keywords: alternative splicing

Query Match 2.9%; Score 176.5; DB 2; Length 793;
Best Local Similarity 18.1%; Pred. No. 0.0002;
Matches 116; Conservative 106; Mismatches 215; Indels 203; Gaps 27;

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QY 555 LKEMSHLETE-----AEARATREAKYERLALDLFSECYSNSERAP----- 596
Db 244 LKELSLVEFRNDYSELAR-----QCKMFAKOLLAQARNRELEVLNHTSDEPLDKR 298
QY 597 ALLVRRNRCSKTTCLHLATEADAKAFADHGVQAFLTRIWMGDMAA--GTPLRLLLGAF 654
Db 299 GLLEER-----MNLRLKLAIKYKQKEFVQSQCQQLNTVWFQMGSGYRKRTCKKIMTV 354
QY 655 LCPALVVTNLTITSEEAFLTGLEDLQDLSLDTSEKSPLYGLQSRVEELVEAPRAQGRG 714
Db 355 LTVGIFW-----PVLISLCYLI-----APKSO----- 375
QY 715 PRAVFLLRWRKFGAPVTVFLGNVVMYFAFLFETVLLVDFRPPPGSPG-----EV 769
Db 376 -----FGRITHTPFMKFIHIGASYFTLLLLNLISLV-YNEDKNTMGPALERIDY 425
QY 770 TLYFWVFLVLEEIRQGFPTDTHLVKKFTLYVGDNNKCDMAVFIPIVGVTCRMLP 828

```


Db 426 LLLILWIGMWSIDIKRLWYEGLED-----FLEESRNQLSFWMSNLYLATFALKVVA 476
QY 829 -----SAFEAGRTVLAMDPMVFT-----LRLIHFAIHKOLGPKIIVVERMM 870
Db 477 HNKPHDFADRKWDADPH--TLVAEGLFAPANVLSYLRFFMYTSSILGLQISMGOQL 534
QY 871 KDV--FFFLFELSVMLVAYGVTTQALLPHDGRLEWIFRRLYRPLQIIF--GOIPLDEI 926
Db 535 QDFGKFLGFLVLVLSFTIGLT-----QYDKGYTSKEOK 569
QY 927 D-----EARVNCSTHPLLEDSPSCPSLYANWLVI-----956
Db 570 DCGVIFCEQSQSNDTHPSFI---GTCFALF--WYIFSLAHVAIFVTRFSYGBELQSFVGA 623
QY 957 LLLVTFLLVTVNLLNMLLIAMFSYTFQVVOGNADMFWRQYNLIVEY-HERPALAPPE- 1014
Db 624 VIVGTYNVVVVLTKLLVAMHLKSFQLIANHEDKEWKFARAKMLSYDFDDKCTLPPPPN 683
QY 1015 -----ILLSHLSLTLLRRVFKAEHKEHLE--RDLPPDQKQVVTWETVQK---- 1059
Db 684 IIPSPKTCYMISSLSKWCISHTSGKVRQNSLKEWRNLKQKRD-----ENYQKVMCC 737
QY 1060 --ENFLSKMEKRRRDEGEVLRTAHRVDVFIKYLGLRE 1097
Db 738 LVHRYLTSRQKQSQSTQATVENLNLQDLSKFRNEIRD 777
RESULT 13
TRPC1 protein - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
C:Accession: I38361
R:Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.
A:Reference number: I38361; MUID:96003837; PMID:7568191
A:Accession: I38361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-810 <RES>
A:Cross-references: EMBL:X89056; NID:g1019786; PID:g1019787
C:Superfamily: TRPC3 protein

Query Match 2.9%; Score 176.5; DB 2; Length 810;
Best Local Similarity 18.1%; Pred. No. 0.0002;
Matches 116; Conservative 106; Mismatches 215; Indels 203; Gaps 27;
QY 555 LKEMSHLETE-----AQAARATREAKYERLALDLFSECYSNBARAF-----596
Db 261 LKELSLVEFRNDYEELAR-----QCKMFAKOLLAQARNSELEVLNHTSSDEPLDKR 315
QY 597 ALLVRNRCSKTTCLHLATEADAKAPFAHDGVAFLTRIWWGDMAA--GTFILRLIGAF 654
Db 316 GLLEER-----MNLRLKLAIKYQKEFVSQSNCOQFLNTWFGOMSGYRKPKCKKIMTV 371
QY 655 LCPALVYTNLITFSEEAPLRTGLEDLQDLSLDEKSPLYGLQSRVEELVEAPQAQDRG 714
Db 372 LTVGIFW-----PVLSLCYLI-----APKSQ-----392
QY 715 PRAVFLTLRWKFWGAPVTVPLGNVVMYFAFLFTVTVLVDPRPPQSGP-----EV 769
Db 393 -----FORIHTPFMKFIHICGASYFTFLLLNLNLSLV--YNEDKNTWGTPALERIDY 442
QY 770 TLYFWVTVLLEERQCFPTD--EDTHLVKFTLVVGNWNNKCDMVAIFLVGTCTRMPL 828
Db 443 LLLILWIGMWSIDIKRLWYEGLED-----FLEESRNQLSFWMSNLYLATFALKVVA 493
QY 829 -----SAFEAGRTVLAMDPMVFT-----LRLIHFAIHKOLGPKIIVVERMM 870
Db 494 HNKPHDFADRKWDADPH--TLVAEGLFAPANVLSYLRFPMTYSSILGLQISMGOQL 551

QY 871 KDV--FFFLFELSVMLVAYGVTTQALLPHDGRLEWIFRRLYRPLQIIF--GOIPLDEI 926
Db 552 QDFGKFLGFLVLVLSFTIGLT-----QYDKGYTSKEOK 586
QY 927 D-----EARVNCSTHPLLEDSPSCPSLYANWLVI-----956
Db 587 DCGVIFCEQSQSNDTHPSFI---GTCFALF--WYIFSLAHVAIFVTRFSYGBELQSFVGA 640
QY 957 LLLVTFLLVTVNLLNMLLIAMFSYTFQVVOGNADMFWRQYNLIVEY-HERPALAPPE- 1014
Db 641 VIVGTYNVVVVLTKLLVAMHLKSFQLIANHEDKEWKFARAKMLSYDFDDKCTLPPPPN 700
QY 1015 -----ILLSHLSLTLLRRVFKAEHKEHLE--RDLPPDQKQVVTWETVQK---- 1059
Db 701 IIPSPKTCYMISSLSKWCISHTSGKVRQNSLKEWRNLKQKRD-----ENYQKVMCC 754
QY 1060 --ENFLSKMEKRRRDEGEVLRTAHRVDVFIKYLGLRE 1097
Db 755 LVHRYLTSRQKQSQSTQATVENLNLQDLSKFRNEIRD 794
RESULT 14
T34472
hypothetical protein W03B1.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34472
R:Miller, N.; Bradshaw, H.; Wu, X.; Gattung, S.
submitted to the EMBL Data Library, June 1998
A:Description: The sequence of C. elegans cosmid W03B1.
A:Reference number: Z21532
A:Accession: T34472
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-823 <MIL>
A:Cross-references: UNIPROT:Q23141; EMBL:U58753; PIDN:AAC24437.1; GSPDB:GN00022; CESP:W03B1
A:Experimental source: Strain Bristol N2; clone W03B1
C:Genetics:
A:Gene: CESP:W03B1.2
A:Map position: 4
A:Introns: 70/3; 102/1; 137/2; 187/2; 265/3; 293/3; 357/3; 489/3; 516/1; 604/2; 628/2
Query Match 2.7%; Score 165; DB 2; Length 823;
Best Local Similarity 22.9%; Pred. No. 0.0014;
Matches 104; Conservative 64; Mismatches 175; Indels 112; Gaps 21;
QY 771 LIPFWTVL-----LEEIRQ---GFTDETHLVKFTLVVGNWNNKCDMVAIFLVIGV 822
Db 406 LAFWRIVLVPLTLEAARLLIFAFVIEKKSSDKNF-----WSGA-----WVLIPI 452
QY 823 TCMLPSAFEAGRTVLAMDPMVFTLRLIHFAIHKOLGPKIIVVERMMKDV-FFFFLFLS 881
Db 453 TLELLYCALPAIAT-----VSTLRFPHSI---QSLGPFHILFKKMKVTGMIFFICT 502
QY 882 VMLVAYGVTTQALLPHDGRLE-----EWIFRRLYRPLQIIFGOIPLDEIDEARV--N 932
Db 503 FWFVL-----AVIHVSISRTLLATNSFLYTVTFQKFEIFGEVQ---DEDIGILLN 552
QY 933 CSTHPLLED-----SPSCPSLYANWLVLVLLVTFLLVTVNLLNMLLIAMFSYTFQV 985
Db 553 CSEYNTKWEFFDMEYAEASC--LFRSTIMPVFYTFVGTILLVNLTAQTKEYENE 610
QY 986 QGNADMFWRQYNLIVEYHERPALAPPEFILL-----1017
Db 611 SKNSAYKGLYKTEQTKIESKLYLPFPFSLFVVLRFWYSCPKYIVITWLTSCCK 670
QY 1018 ---SHLSLTLLRRVFKAEHKEHLE--RDLPPDQKQVVTWETVQKFNLSKME-----K 1068
Db 671 CSSTAISLWYRNIIVRIVEGYPGAVRQTDNEIDTKVAEFLRKRPNDALEKDLVNNYD 730
QY 1069 RRDSEGEVLRTAHRV-DFIKYLGLREQEKRIKLESQINVCYSLVSSVADVLQGG 1127
Db 731 KDVDDE-EALKGLGKEIKKFLAKEIG--EBEREAQSNLENHPRSGSVLDPKKHRLS--- 784

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OM protein - protein search, using sw model

Run on: June 22, 2005, 18:08:14 ; Search time 192 Seconds
(without alignments)
3107.147 Million cell updates/sec

Title: US-09-834-792D-4
Perfect score: 6093
Sequence: 1 MQDVQPRPGSGDAEDRRE.....HRGGLDGWEQPGAGQPPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_prot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6093	100.0	1165	Q9NZQ8	Q9NZQ8 homo sapien
2	6039	99.1	1159	Q9NY34	Q9NY34 homo sapien
3	5088.5	83.5	1158	Q9JUH7	Q9JUH7 mus musculus
4	5036.5	82.7	1148	Q9EPM4	Q9EPM4 mus musculus
5	5026.5	82.5	1148	Q99NF9	Q99NF9 mus musculus
6	4981.5	81.8	1116	Q9EPM3	Q9EPM3 mus musculus
7	4465.5	73.3	1030	Q8BS44	Q8BS44 m mus muscu
8	4354.5	71.5	1000	Q7TFL4	Q7TFL4 mus musculus
9	2448.5	40.2	1214	Q8TD43	Q8TD43 homo sapien
10	2399.5	39.4	1213	Q7TN37	Q7TN37 mus musculus
11	2184.5	35.9	1040	Q96L84	Q96L84 homo sapien
12	2164	35.5	1016	Q9NXV1	Q9NXV1 homo sapien
13	2098	34.4	1069	Q7ZSD9	Q7ZSD9 homo sapien
14	2069	34.0	945	Q8BLM7	Q8BLM7 mus musculus
15	2039	33.5	1503	1 TRL2 HUMAN	Q94759 homo sapien
16	2021	33.2	1507	Q91YD4	Q91YD4 mus musculus
17	1924.5	31.6	872	Q6PDM0	Q6PDM0 mus musculus
18	1722	28.3	793	Q80Y94	Q80Y94 mus musculus
19	1582	26.0	1104	Q8RAD5	Q8RAD5 mus musculus
20	1579.5	25.9	779	Q7TOW9	Q7TOW9 xenopus lae
21	1567.5	25.7	1104	Q8RA55	Q8RA55 rattus norv
22	1565.5	25.7	1104	Q7Z2W7	Q7Z2W7 homo sapien
23	1563.5	25.7	1095	Q8TDX8	Q8TDX8 homo sapien
24	1563.5	25.7	1104	Q8TAC3	Q8TAC3 homo sapien
25	1534.5	21.9	1718	Q69ZB8	Q69ZB8 mus musculus
26	1312.5	21.7	1325	Q8EUL0	Q8EUL0 homo sapien
27	1312.5	21.5	1566	Q86WK3	Q86WK3 homo sapien
28	1307.5	21.5	1544	Q86WK2	Q86WK2 homo sapien
29	1307.5	21.5	1544	Q86Z00	Q86Z00 homo sapien
30	1307.5	21.5	1554	Q86SH6	Q86SH6 homo sapien
31	1303.5	21.4	1556	Q86WK1	Q86WK1 homo sapien

32 1303.5 21.4 1566 2 Q86WK4
33 1300 21.3 1569 2 Q86Z01
34 1300 21.3 1579 2 Q86SH0
35 1286.5 21.1 846 2 Q6J3P5
36 1251.5 20.5 1526 2 Q86Y29
37 1242.5 20.4 1527 2 Q7Z4N1
38 1240.5 20.4 1533 2 Q75560
39 1240.5 20.4 1533 2 Q7Z4N2
40 1240.5 20.4 1533 2 Q7Z4N5
41 1239.5 20.3 1533 2 Q7Z4N4
42 1225 20.1 1070 2 Q7PT99
43 1214.5 19.9 1862 2 Q925B2
44 1214.5 19.9 1863 2 Q923J1
45 1214.5 19.9 1863 2 Q9JLQ1

ALIGNMENTS

RESULT 1

Q9NZQ8 PRELIMINARY; PRT; 1165 AA.
AC Q9NZQ8;
DT 01-OCT-2000 (Tremblrel..15, Created)
DT 01-OCT-2000 (Tremblrel..15, Last sequence update)
DT 01-MAR-2004 (Tremblrel..26, Last annotation update)
DE MTR1.
GN Name=MTR1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20076317; PubMed=10607831; DOI=10.1093/hmg/9.2.203;
RA Prawitt D., Enklaar T., Klemm G., Gaertner B., Spangenberg C., Winterpacht A., Higgins M., Pelletier J., Zabel B.;
RT "Identification and characterization of MTR1, a novel gene with homology to melastatin (MLSN1) and the trp gene family located in the BWS-WT2 critical region on chromosome 11p15.5 and showing allele-specific expression.";
RL Hum. Mol. Genet. 9:203-216(2000).
DR EMBL; AF177473; AAF26288.1; -.
DR Genbank; HGNC:14323; TRPMS.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR GO; GO:0005216; F: ion channel activity; TAS.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 1165 AA; 131450 MW; C4AD5BAA866BE73B CRC64;
Query Match 100.0%; Score 6093; DB 2; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQDVQPRPGSGDAEDRRELGLHGEVNFVGGSGKKRGKRVFVPSGVAFLDLLAEW 60
DB 1 MQDVQPRPGSGDAEDRRELGLHGEVNFVGGSGKKRGKRVFVPSGVAFLDLLAEW 60
QY 61 HLPAPNLVSVLGEQPFAMKSLRDVLRKGLVKAAQSTGAWILTSALRVGLARHVQAV 120
DB 61 HLPAPNLVSVLGEQPFAMKSLRDVLRKGLVKAAQSTGAWILTSALRVGLARHVQAV 120
QY 121 RHSLASTSTKRVAVAGMASLGRVLRHRLIEEAQEDFPVHPEDDGGSGGLCSLDNL 180
DB 121 RHSLASTSTKRVAVAGMASLGRVLRHRLIEEAQEDFPVHPEDDGGSGGLCSLDNL 180
QY 181 SHFILLVEPPGPGKDGGLTELRLRLEKHSIQAGYGTSGSIEIPVLCILVNGDPNTERI 240
DB 181 SHFILLVEPPGPGKDGGLTELRLRLEKHSIQAGYGTSGSIEIPVLCILVNGDPNTERI 240
QY 241 SRAVEQAAPWLILVGGGDIADVLALVNQPHLLVPPKVAEKQPKFKFSWEDIVRW 300

Db 241 SRAVEQAAPWLLVSGGGIADVLAAVLPVQPHLLVPKVAEKQKFKPSKHSFVWVMT 300
 Qy 301 KLLQNTSHQHLITVDFEQSGSEELDTVILKALVKACKSHSQBPQDYDLKLA VAWDR 360
 Db 301 KLLQNTSHQHLITVDFEQSGSEELDTVILKALVKACKSHSQBPQDYDLKLA VAWDR 360
 Qy 361 VDIKSEIFNGDVEWKSCDLEVMVDALVSNKPEFVRLFDNGADVADFLTYGRLOELYL 420
 Db 361 VDIKSEIFNGDVEWKSCDLEVMVDALVSNKPEFVRLFDNGADVADFLTYGRLOELYL 420
 Qy 421 SVSRKSLFLLQKQKEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLVKDFLQDACRG 480
 Db 421 SVSRKSLFLLQKQKEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLVKDFLQDACRG 480
 Qy 481 FYQDGRPDGRRRAEKGPAPKPTGQKWLDDLNQKSENPMWDLFLWAVLQNRHEMATYFWAM 540
 Db 481 FYQDGRPDGRRRAEKGPAPKPTGQKWLDDLNQKSENPMWDLFLWAVLQNRHEMATYFWAM 540
 Qy 541 GOEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLV 600
 Db 541 GOEGVAAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLV 600
 Qy 601 RNRKWSKTTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAAGTPILRLILGALFLCPALV 660
 Db 601 RNRKWSKTTCLHLATEADAKAFPAHDGVQAFTRIWMGDMAAGTPILRLILGALFLCPALV 660
 Qy 661 YTNLITFSEAPLRTGLDQLDLSLDTKESPLVGLQSRVVELVEAPRAQGDGRPRAVFL 720
 Db 661 YTNLITFSEAPLRTGLDQLDLSLDTKESPLVGLQSRVVELVEAPRAQGDGRPRAVFL 720
 Qy 721 LTRWRKFGAPVTVFVGNVVMYFAPLFTVVLAVDRPPQSGSGPEVTLYFWVFTVLV 780
 Db 721 LTRWRKFGAPVTVFVGNVVMYFAPLFTVVLAVDRPPQSGSGPEVTLYFWVFTVLV 780
 Qy 781 BEIRQGFPTDDBTHLVKKFTLVVGNMKNKDMVAIFLFIIVGVTCTRMPLPSAFEAGRTVLAM 840
 Db 781 BEIRQGFPTDDBTHLVKKFTLVVGNMKNKDMVAIFLFIIVGVTCTRMPLPSAFEAGRTVLAM 840
 Qy 841 DPMVFTLRLIHFALHKGQKPIIVVERMKDVFVFLFVLVAVGVTTQALLHPHDG 900
 Db 841 DPMVFTLRLIHFALHKGQKPIIVVERMKDVFVFLFVLVAVGVTTQALLHPHDG 900
 Qy 901 RLEWIFRVLRYPLQIFQGLPDEIDEARVNCSTHPLLEDSPSCSLYANWLVILLV 960
 Db 901 RLEWIFRVLRYPLQIFQGLPDEIDEARVNCSTHPLLEDSPSCSLYANWLVILLV 960
 Qy 961 TFLVTVNVLNLLIAMPSYTFQVVGADMFVQRYNLIYVHERPALAPPFILLSHL 1020
 Db 961 TFLVTVNVLNLLIAMPSYTFQVVGADMFVQRYNLIYVHERPALAPPFILLSHL 1020
 Qy 1021 SLTLRRVPKKAHKEHLEHRLDPLDQKVVTWETVQKFNFLSKMEKRRDSEGEVLK 1080
 Db 1021 SLTLRRVPKKAHKEHLEHRLDPLDQKVVTWETVQKFNFLSKMEKRRDSEGEVLK 1080
 Qy 1081 TAHRVDFTAFLYGLGRLEKEIKLESQINVCVSVLVSSVADVLAQGGGPRSSQCHGSGSQ 1140
 Db 1081 TAHRVDFTAFLYGLGRLEKEIKLESQINVCVSVLVSSVADVLAQGGGPRSSQCHGSGSQ 1140
 Qy 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165
 Db 1141 LVAADHRGGLDGEQPGAGQPPSDT 1165

RESULT 2

Q9NY34 ID Q9NY34 PRELIMINARY; PRT: 1159 AA.
 AC Q9NY34;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE LTRPCS protein (fragment).
 GN Name=LTRPCS;

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paulsen M., El-Waari O., Engemann S., Franck O., Stroedicke M.,
 RA Davies K.R., Bowden L.M., Reinhardt R., Reik W., Harteneck C.,
 RA Walter J.,
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ270996; CAB66342.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Ion_trans.
 DR KW Ion transport; Ionic channel; Transmembrane; Transport.
 FT NON TER 1
 SQ SEQUENCE 1159 AA; 130774 MW; E31658C1125363B CRC64;
 Query Match 99.1%; Score 6039; DB 2; Length 1159;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1157; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
 Qy 9 PGSPGDAEDREELGLHGRGEVNFQSGKKCKGKFRVPSGVAPSVLFDLLAEWHLPAVNV 68
 Db 1 PGSPGDAEDREELGLHGRGEVNFQSGKKCKGKFRVPSGVAPSVLFDLLAEWHLPAVNV 60
 Qy 69 VSLVGEQPPAMKSWLDRVLRKGLVKAQAQSTGAWILTSALRVGLARHVGAQVDRHSLAST 128
 Db 61 VSLVGEQPPAMKSWLDRVLRKGLVKAQAQSTGAWILTSALRVGLARHVGAQVDRHSLAST 120
 Qy 129 STKRVVAVGMASIGRVLHRRILIEEAQ--EDFPVHYPEDDGGSGQPLCSLDSNLSHFV 186
 Db 121 STKRVVAVGMASIGRVLHRRILIEEAQVHEDFPVHYPEDDGGSGQPLCSLDSNLSHFV 180
 Qy 187 EPQPPGKGGDLTELRLEKHSIQRAGYGGTGSIEIPVLCLLVNGDPNLTISRIVEQ 246
 Db 181 EPQPPGKGGDLTELRLEKHSIQRAGYGGTGSIEIPVLCLLVNGDPNLTISRIVEQ 240
 Qy 247 AAPWLLVSGGGIADVLAAVLPVQPHLLVPKVAEKQKFKPSKHSFVWVMTVTKLQNI 306
 Db 241 AAPWLLVSGGGIADVLAAVLPVQPHLLVPKVAEKQKFKPSKHSFVWVMTVTKLQNI 300
 Qy 307 TSHQHLITVDFEQSGSEELDTVILKALVKACKSHSQBPQDYDLKLA VAWDRVDIAKS 366
 Db 301 TSHQHLITVDFEQSGSEELDTVILKALVKACKSHSQBPQDYDLKLA VAWDRVDIAKS 360
 Qy 367 EIFNGDVEWKSCDLEVMVDALVSNKPEFVRLFDNGADVADFLTYGRLOELYSVSRKS 426
 Db 361 EIFNGDVEWKSCDLEVMVDALVSNKPEFVRLFDNGADVADFLTYGRLOELYSVSRKS 420
 Qy 427 LLDLQKQKEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLVKDFLQDACRGFYQDGR 486
 Db 421 LLDLQKQKEEARLTLAGLGTQQAAREPPAGPPAFSLHEVSVLVKDFLQDACRGFYQDGR 480
 Qy 487 PGDRRAEKGPAPKPTGQKWLDDLNQKSENPMWDLFLWAVLQNRHEMATYFWAMGEGVA 546
 Db 481 PGDRRAEKGPAPKPTGQKWLDDLNQKSENPMWDLFLWAVLQNRHEMATYFWAMGEGVA 540
 Qy 547 AALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLVRRNCW 606
 Db 541 AALAAACKILKEMSHLETEAARATREAKYERLALDLFSECYSNSEARAFALLVRRNCW 600
 Qy 607 SKTTCCLHLATEADAKAFPAHDGVQAFTRIWMGDMAAGTPILRLILGALFLCPALVYTNLIT 666
 Db 601 SKTTCCLHLATEADAKAFPAHDGVQAFTRIWMGDMAAGTPILRLILGALFLCPALVYTNLIT 660
 Qy 667 FSEAPLRTGLDQLDLSLDTKESPLVGLQSRVVELVEAPRAQGDGRPRAVFLTRWRK 726
 Db 661 FSEAPLRTGLDQLDLSLDTKESPLVGLQSRVVELVEAPRAQGDGRPRAVFLTRWRK 720

QY 727 FWGAPVTVFLGNVVMYFAFLFTYVLLVDRPPPPQSGPGEVLYFWVFTLVLEEIRQG 786
DB 721 FWGAPVTVFLGNVVMYFAFLFTYVLLVDRPPPPQSGPGEVLYFWVFTLVLEEIRQG 780
QY 787 FTTDDTHLVKKFTLYVGDNNKCDMVAIFLIVGVTCTMLPSAFAEAGRTVLANDFWVFT 846
DB 781 FTTDDTHLVKKFTLYVGDNNKCDMVAIFLIVGVTCTMLPSAFAEAGRTVLANDFWVFT 840
QY 847 LRLHIFAIHQGLGPKIIIVVERMKDVFELFELSLVAVGVTTQALLHPDGRLEWIF 906
DB 841 LRLHIFAIHQGLGPKIIIVVERMKDVFELFELSLVAVGVTTQALLHPDGRLEWIF 900
QY 907 RRVLYRPVLOIQQIPLDEIDVNCSTHPLLEDSPSCPSLYANMLVILLVFTLLV 966
DB 901 RRVLYRPVLOIQQIPLDEIDVNCSTHPLLEDSPSCPSLYANMLVILLVFTLLV 960
QY 967 NVLLMNLIIAMPSYTFQVQVGNADMFWKFORVNLIVYHERPALAPPFILLSHLSLTLRR 1026
DB 961 NVLLMNLIIAMPSYTFQVQVGNADMFWKFORVNLIVYHERPALAPPFILLSHLSLTLRR 1020
QY 1027 VPKKAHREHLERDLDPDLQKVVTWETQKENFLSKMEKRRDSEGEVLRTAHRVD 1086
DB 1021 VPKKAHREHLERDLDPDLQKVVTWETQKENFLSKMEKRRDSEGEVLRTAHRVD 1080
QY 1087 FTAKYLGGLREOEKIKLESQINYSVLVSSVADVLQGGGPRSSQHCQEGSOLVAADH 1146
DB 1081 FTAKYLGGLREOEKIKLESQINYSVLVSSVADVLQGGGPRSSQHCQEGSOLVAADH 1140
QY 1147 RGLDGEQPGAGQPPSDT 1165
DB 1141 RGLDGEQPGAGQPPSDT 1159
RESULT 3
Q9JUH7 PRELIMINARY; PRT; 1158 AA.
AC Q9JUH7
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE MSLN1-and TRP-related protein 1 (MTR1) (Transient receptor potential
cation channel subfamily M member 5).
GN Name=Trpm5; Synonyms=Mtr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20363096; PubMed=10907850;
RA Yatsuki H., Watanabe H., Hattori M., Joh K., Soejima H., Komoda H.,
RA Xin Z., Zhu X., Higashimoto K., Nishimura M., Kuratomi S., Sasaki H.,
RA Sakaki Y., Mukai T.;
RT "Sequence-based structural features between Kv1qt1 and Tapal on mouse
chromosome 7P4/P5 corresponding to the Beckwith-Wiedemann syndrome
region on human 1p15.5: long-stretches of unusually well conserved
intronic sequences of Kv1qt1 between mouse and human.";
RL DNA Res. 7:195-206 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20366135; PubMed=10903843; DOI=10.1006/geno.2000.6234;
RA Enklaar T., Esswein M., Oswald M., Hilbert K., Winterpacht A.,
RA Higgins M., Zabel B., Prawitt D.;
RT "Mtr1, a novel biallelically expressed gene in the center of the mouse
distal chromosome 7 imprinting cluster, is a member of the Trp gene
family.";
RL Genomics 67:179-187 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvxC57BL; TISSUE=Lung;
RX MEDLINE=2276392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
RA Hofmann T., Chubakov V., Gudermann C., Montell C.;
RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent

selective cation channel.";
RL Curr. Biol. 13:1153-1158 (2003).
DR EMBL; AB019952; BAA96877.1; -
DR EMBL; AF228681; AAF98120.1; -
DR EMBL; AY280364; AAP44476.1; -
DR MGD; MGI:1861718; trpm5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKTRIN.
KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
SQ SEQUENCE 1158 AA; 130843 MW; FOA5237EC67867CE CRC64;
Query Match 83.5%; Score 5088.5; DB 2; Length 1158;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 982; Conservative 67; Mismatches 106; Indels 13; Gaps 4;
QY 1 MODVQGRPGSPGDAEDRRRLGLHRGEVNFSGGKRGKFKVRVPSGVAPS VLFLLLLAEW 60
DB 1 MOTTQSSCPGPPPTDGDWEPILCRGEINFGSGKRGKFKVRVSSVAPS VLFLLLTETW 60
QY 61 HLPAPNLVSLVSGEQPFAMKSWLRDLVRLKGLVKAQSTGAWILTSALRVGLARHVGOAV 120
DB 61 HLPAPNLVSLVSGEERPLAMKSWLRDLVRLKGLVKAQSTGAWILTSALRVGLARHVGOAV 120
QY 121 RDHSLASTSTKVRVAVGMASLGRVLRRIULE--EAQEDFPVHPYEDDGGSGGGLCSLDS 178
DB 121 RDHSLASTSTKIRVVAIGMASLDRILHRQLLDGVHQKEDTPIHYPADEGNIQGPLCLDS 180
QY 179 NLSHFILVEPQPGKG-DGLTELRLLEKHISEORAGYGGTGSTIEI PVLCLLVNGDPNTL 237
DB 181 NLSHFILVESGALSGNDGLTELQLSLEKHISQORTGYGGTSCIQIPVLCLLVNGDPNTL 240
QY 238 ERISRAVEQAAAPWLLITVSGGGIADVLAALVNPQPHLLVPKVAEKQFKKFPKSHFSEWIDV 297
DB 241 ERISRAVEQAAAPWLLIAGSGGIADVLAALVNPQPHLLVPKVAEKQFKKFPKSHFSEWIDV 300
QY 298 RWTLLQNTITSHOHLITVYDFEQEGSELDITVILKALVKACKSHSQEODYLDLKLAVA 357
DB 301 HWTLLQNTIAAHPHLLITVYDFEQEGSELDITVILKALVKACKSHSQEODYLDLKLAVA 360
QY 358 WDRVDIAKSEIFNGDVEWVKSCDLEEVYDALVSNKPEFVRLVDNGADVADFLTYGRLOE 417
DB 361 WDRVDIAKSEIFNGDVEWVKSCDLEEVYDALVSNKPEFVRLVDNGADVADFLTYGRLOE 420
QY 418 LYRSVSRKSLFLDLLQKQOEARLTLAGLTQQAEPAGPPAFSLHEVSRVLKDFLODA 477
DB 421 LYHSVSPKSLFLDLLQKQOEGRULTLAGLQQAQARELPGLPAPSLHEVSRVLKDFLODA 480
QY 478 CRGFYQDGRPGDRRRAEKGPAKPTGQKWLDLNOKSNPNWRDLFLMAVLQNRHEMATYF 537
DB 481 CRGFYQDQ-----RRMEERGPKPAGQKWLPLDSKSDPNWRDLFLMAVLQNRHEMATYF 536
QY 538 WAMQEGVAAALAAACKILKEMSHLSEAEAPATREAKYERLALDLFSECYNSSEARAPA 597
DB 537 WAMQEGVAAALAAACKILKEMSHLSEAEAVARTMEAKYEQALDLFSECYNSSEARAPA 596
QY 598 LLVVRNCRWSTKTCILHATEADAKAFFAHGDVQOAFTRIWMGDMAGTPIRLLLGAFCLCP 657
DB 597 LLVVRNHSRSTKTCILHATEADAKAFFAHGDVQOAFTRIWMGDMATGPIRLLLGAFCLCP 656
QY 658 ALVYTNLITFSEAPLRTGLEDLQDLSDTEKSPLYGLQSRVEELVEAPRAGGRGPPA 717
DB 657 ALIYTNLITFSEAPLRTGLEDLQDLSDTEKSPLYGLQSRVEELVEAPRAGGRGPPA 716
QY 718 VFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDRPPPPQSGPGEVLYFWVFT 777
DB 717 AFLLTRWRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDRPPPPQSGPGEVLYFWVFT 776

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QY 778 LVLEIRQGFDTEDTHLVKKFTLYVGDNNKCDMVAIFLFIYGVTCRMLPSAFEAGRTV 837
DB 777 LVLEIRQGFDTEDTHLVKKFTLYVEDNNKCDMVAIFLFIYGVTCRMVPSFEAGRTV 836
QY 838 LAMDPMVFTLRLLIHFIAHKQLGPKIIVVERMKDVFFFLFSLVNLVAYGVTTQALLHP 897
DB 837 LAIDPMVFTLRLLIHFIAHKQLGPKIIVVERMKDVFFFLFSLVNLVAYGVTTQALLHP 896
QY 898 HDGRLEWIFRRVLYRPLQIFQGIPLDEIDEARVNCSTHPLLEDSPSPSIYANWLVL 957
DB 897 HDGRLEWIFRRVLYRPLQIFQGIPLDEIDEARVNCSTHPLLEDSPSPSIYANWLVL 956
QY 958 LLVTFLLVTNVLNLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPPFILL 1017
DB 957 LLVTFLLVTNVLNLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPPFILL 1016
QY 1018 SHLSLTLRRVPKKEAEKREHLERDLPDLDQKVVTWETVQKFNFLSKMEKRRRDEGEV 1077
DB 1017 SHLSLVLQVFRKEAQHRLERDLPDLDQKIIITWETVQKFNFLSKMEKRRRDEGEV 1076
QY 1078 LRKTAHRVDFIAKYLGLREQEKRIKLESQINYSVLSSVADVLAQGGPRSSQHCGE 1137
DB 1077 LRKTAHRVLLIAKYLGLREQEKRIKLESQINYSVLSSVADVLAQGGPRSSQHCGE 1136
QY 1138 GSQVLAADHRGDLGWEPGAGOPPBDT 1165
DB 1137 RSQPASARDREYLE-----SGLPPSDT 1158

RESULT 4
Q9EPM4 PRELIMINARY; PRT; 1148 AA.
AC Q9EPM4;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Ltrpc5 protein.
GN Name=ltrpc5; Synonyms=Ltrpc5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX PubMed=10915772; DOI=10.1093/hmg/9.12.1829;
RA Paulsen M., El-Mearri O., Engemann S., Stroedicke M., Franck O.,
RA Davies K., Reinhardt R., Reik W., Walter J.;
RT "Sequence conservation and variability of imprinting in the Beckwith-
RT Wiedemann syndrome gene cluster in human and mouse.";
RL Hum. Mol. Genet. 9:1829-1841 (2000).
DR EMBL; AJ251835; CAC19456.1; -.
DR MGD; MGI:1861718; Trpm5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR Pfam; PF00520; Ion trans.
DR PRINTS; PR01415; ANKVRIN.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 1148 AA; 129630 MW; 94AF5B9CFDCA127 CRC64;

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Query Match      82.7%; Score 5036.5; DB 2; Length 1148;
Best Local Similarity 85.5%; Pred. No. 0;
Matches 966; Conservative 63; Mismatches 94; Indels 7; Gaps 3;

QY 1 MQDVGGPPGSGDAEDRELGLHGEVNFQSGSKRGKRVPSGVAPSLFDLLAEW 60
DB 1 MQTVSSCGSPDPDTEGWEPILCRGEINFGSGSKRGKRVPSGVAPSLFELLITEW 60

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QY 61 HLPAPNLVSVLVBGEQPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRYGLARHVQAV 120
DB 61 HLPAPNLVSVLVBGEQPFAMKSWLRDLVRKGLVKAAQSTGAWILTSALRYGLARHVQAV 120
QY 121 RDHSLASTSTKRVVAVGMASLGRVLAHRRILE--EAGEDFVHYHPEDDGGSQPLCLSDS 178
DB 121 RDHSLASTSTKRVVAVGMASLGRVLAHRRILE--EAGEDFVHYHPEDDGGSQPLCLSDS 178
QY 179 NLSHFILVEPQPGKG-DGLTELRRLRLEKHSIORAGYGGTGTETIEIPVLCLLVNGDPNTL 237
DB 181 NLSHFILVESGALSGNDGLTEQLSLEKHSIORAGYGGTGTETIEIPVLCLLVNGDPNTL 240
QY 238 ERISRAVQQAAPWILLVSGGIADVLAAVNQPHLLVPKVAEKQFKEKPSKHSFMSMEDIV 297
DB 241 ERISRAVQQAAPWILLVSGGIADVLAAVNQPHLLVPKVAEKQFKEKPSKHSFMSMEDIV 297
QY 298 RWTXLLQNIITSHOHLITVYDFEBOGSEELDTVLKALVKACKSHSOBQDYLDELKAVA 357
DB 301 HWTXLLQNIITSHOHLITVYDFEBOGSEELDTVLKALVKACKSHSOBQDYLDELKAVA 360
QY 358 WDRVDIAKSEIFNGDVENKSCDLEEVMTDALVSNKPDFVRLPVDSCADMAEFITYGLQQ 417
DB 361 WDRVDIAKSEIFNGDVENKSCDLEEVMTDALVSNKPDFVRLPVDSCADMAEFITYGLQQ 420
QY 418 LYRSVSRKSLLDLQKQKOEAEELTLAGLGTQOAREPPAGPPAPSPAPSLHEVSRVLKDFLQDA 477
DB 421 LYHSVSPKSLFELLQKQKHEBRLTLAGLGAQOARELPTGLPAPSLHEVSRVLKDFLQDA 480
QY 478 CRGFYQDGRFRRRAEKGPFAKPTQKWLLOLNQSENPNRDLPLWAVLQNRHEMATYF 537
DB 481 CRGFYQDGRFRRRAEKGPFAKPTQKWLLOLNQSENPNRDLPLWAVLQNRHEMATYF 536
QY 538 WANGQGVAAALAAACKILKEMSHLETEAARATREAKYERIALDLFSYCSNSEARAPA 597
DB 537 WANGQGVAAALAAACKILKEMSHLETEAARATREAKYERIALDLFSYCSNSEARAPA 596
QY 598 LLVRRNRCWSKTTCLHLATEADAKAFHAGDQVQAFTRIWMGDMAAGTPIRLIAGFLCP 657
DB 597 LLVRRNHSWSRTTCLHLATEADAKAFHAGDQVQAFTRIWMGDMAAGTPIRLIAGFLCP 656
QY 658 ALVYTNLIITFSEAPLRTGLELDLQDLSLDTBKSPLYGLQSRVEBELVEAPRAGQGRGPA 717
DB 657 ALVYTNLISFSEDAPOQMDLEDLQBPDSLDMEKSLCSRGQGLEKITEAPRAPDGLGQA 716
QY 718 VELLTRWRKFWGAPVTVFIGNVVMYFAFLFTYVLLVDPRPPQPGSPGPEVTLFWVPT 777
DB 717 AFLTRWRKFWGAPVTVFIGNVVMYFAFLFTYVLLVDPRPPQPGSPGPEVTLFWVPT 776
QY 778 LVLEIRQGFDTEDTHLVKKFTLYVGDNNKCDMVAIFLFIYGVTCRMLPSAFEAGRTV 837
DB 777 LVLEIRQGFDTEDTHLVKKFTLYVEDNNKCDMVAIFLFIYGVTCRMVPSFEAGRTV 836
QY 838 LAMDPMVFTLRLLIHFIAHKQLGPKIIVVERMKDVFFFLFSLVNLVAYGVTTQALLHP 897
DB 837 LAIDPMVFTLRLLIHFIAHKQLGPKIIVVERMKDVFFFLFSLVNLVAYGVTTQALLHP 896
QY 898 HDGRLEWIFRRVLYRPLQIFQGIPLDEIDEARVNCSTHPLLEDSPSPSIYANWLVL 957
DB 897 HDGRLEWIFRRVLYRPLQIFQGIPLDEIDEARVNCSTHPLLEDSPSPSIYANWLVL 956
QY 958 LLVTFLLVTNVLNLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPPFILL 1017
DB 957 LLVTFLLVTNVLNLLIAMFSYTFQVQGNADMFWKFORYNLIVEYHERPALAPPFILL 1016
QY 1018 SHLSLTLRRVPKKEAEKREHLERDLPDLDQKVVTWETVQKFNFLSKMEKRRRDEGEV 1077
DB 1017 SHLSLVLQVFRKEAQHRLERDLPDLDQKIIITWETVQKFNFLSKMEKRRRDEGEV 1076
QY 1078 LRKTAHRVDFIAKYLGLREQEKRIKLESQINYSVLSSVADVLAQGG 1127
DB 1077 LRKTAHRVLLIAKYLGLREQEKRIKLESQINYSVLSSVADVLAQGG 1126

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RESULT 5
Q99NF9 PRELIMINARY; PRT; 1148 AA.
ID Q99NF9;
AC Q99NF9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ltrpc5 protein.
GN Name=Ltrpc5; Synonyms=Ltrpc5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX PubMed=10915772; DOI=10.1093/hmg/9.12.1829;
RA Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O.,
RA Davies K., Reinhardt R., Reik W., Walter J.;
RT "Sequence conservation and variability of imprinting in the Beckwith-
RT Wiedemann syndrome gene cluster in human and mouse.";
RL Hum. Mol. Genet. 9:1829-1841(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX Engemann S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271092; CAB94717.2; -.
DR MGD; MGI:1861718; Trpm5.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR005821; Ion trans.
DR Pfam; PF00520; Ion trans. 1.
DR PRINTS; PR01415; ANKVRIN.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW SEQUENCE 1148 AA; 129590 MW; 90517E8557DCA127 CRC64;

Query Match 82.5%; Score 5026.5; DB 2; Length 1148;
Best Local Similarity 85.4%; Pred. No. 0;
Matches 965; Conservative 63; Mismatches 95; Indels 7; Gaps 3;

QY 1 MQDVQGRPGSGDAEDRELGLHREGVNPGSGKRGKFRVPSGVAISVFLDLLAEW 60
DB 1 MQTTQSSCPGSPDTEGWEPILCRGEINFGSGKRGKFRVPSVAPSVLPELLTEW 60

QY 61 HLPAPNLVSLVGEERPFANKSWLRDVLKGLVKAQSTGAWILTSALRVGLARHVGQAV 120
DB 61 HLPAPNLVSLVGEERPLANKSWLRDVLKGLVKAQSTGAWILTSALRVGLARHVGQAV 120

QY 121 RDHSLASTSKRVAVGMSLGRVLRILE--EAQEDPPVHYPPEDDGGSGPLCLSDS 178
DB 121 RDHSLASTSKRVAVGMSLGRVLRILE--EAQEDPPVHYPPEDDGGSGPLCLSDS 178

QY 121 RDHSLASTSKRVAVGMSLGRVLRILE--EAQEDPPVHYPPEDDGGSGPLCLSDS 180
DB 121 RDHSLASTSKRVAVGMSLGRVLRILE--EAQEDPPVHYPPEDDGGSGPLCLSDS 180

QY 179 NLSHFILVPEPGKGG--DGLTELRLEKHSIQRAGYGTGSIPIVCLLVNGDPNTL 237
DB 179 NLSHFILVPEPGKGG--DGLTELRLEKHSIQRAGYGTGSIPIVCLLVNGDPNTL 237

QY 181 NLSHFILVPEPGKGG--DGLTELRLEKHSIQRAGYGTGSIPIVCLLVNGDPNTL 240
DB 181 NLSHFILVPEPGKGG--DGLTELRLEKHSIQRAGYGTGSIPIVCLLVNGDPNTL 240

QY 238 ERISRAVEQAAPMLILVSGSGIADVLAAVYNQPHLLVPKVAEKQPKPKSHFSMEDIV 297
DB 238 ERISRAVEQAAPMLILVSGSGIADVLAAVYNQPHLLVPKVAEKQPKPKSHFSMEDIV 297

QY 241 ERISRAVEQAAPMLILVSGSGIADVLAAVYNQPHLLVPKVAEKQPKPKSHFSMEDIV 300
DB 241 ERISRAVEQAAPMLILVSGSGIADVLAAVYNQPHLLVPKVAEKQPKPKSHFSMEDIV 300

QY 298 RWTLLQNTSHOHLTYDPEQSGSELDVTILKALVKACKSHSQPQDYDLDELKAVA 357
DB 298 RWTLLQNTSHOHLTYDPEQSGSELDVTILKALVKACKSHSQPQDYDLDELKAVA 357

QY 301 HWTLLQNTSHOHLTYDPEQSGSELDVTILKALVKACKSHSQPQDYDLDELKAVA 360
DB 301 HWTLLQNTSHOHLTYDPEQSGSELDVTILKALVKACKSHSQPQDYDLDELKAVA 360

QY 358 WDRVDIAKSEIFNGDVEWKSCDLEEVNMDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 417
DB 358 WDRVDIAKSEIFNGDVEWKSCDLEEVNMDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 417

QY 361 WDRVDIAKSEIFNGDVEWKSCDLEEVNMDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 420
DB 361 WDRVDIAKSEIFNGDVEWKSCDLEEVNMDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 420

QY 418 LYRSVSRKSLFDLLQKKEEARLTLAGLGTQQAREPPAGPPAPSLHEVSRVLKDFLQDA 477
DB 418 LYRSVSRKSLFDLLQKKEEARLTLAGLGTQQAREPPAGPPAPSLHEVSRVLKDFLQDA 477

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DB 421 LYHSVSPKSLFELLQKKEEARLTLAGLGTQQAREPPAGPPAPSLHEVSRVLKDFLQDA 480
QY 478 CRGYQDGRPGDRAAEKPAKRTGQKWLIDLNLKSENPRDLFLWAVLQNRHEMATYF 537
DB 481 CRGYQDGRPGDRAAEKPAKRTGQKWLIDLNLKSENPRDLFLWAVLQNRHEMATYF 536
QY 538 WAMQEGVAAALAAACKILKEMSHLETEAEARATREAKYERLALDLSECYNSSEARAF 597
DB 537 WAMQEGVAAALAAACKILKEMSHLETEAEARATREAKYERLALDLSECYNSSEARAF 596
QY 598 LLVPRNCWSKTTCLHLATEADAKAFHAGDGVQAFLTRIWMGDMAAGTPILRLILGAF 657
DB 597 LLVPRNCWSKTTCLHLATEADAKAFHAGDGVQAFLTRIWMGDMAAGTPILRLILGAF 656
QY 658 ALVVTNLITFSEAPLRTGLDQLDLSLDTPEKSLYGLQSRVEELVEAPRAQDGRGPA 717
DB 657 ALVVTNLITFSEAPLRTGLDQLDLSLDTPEKSLYGLQSRVEELVEAPRAQDGRGPA 716
QY 718 VFLTRWRKFWGAPVTVFLGNVNVYFAPLFTVTVLLVDFRPPQPGSGPEVTLYFWYFT 777
DB 717 VFLTRWRKFWGAPVTVFLGNVNVYFAPLFTVTVLLVDFRPPQPGSGPEVTLYFWYFT 776
QY 778 LVLEIRQGFPTDTHLVKFTLYVGNWNKCDWVAIFLIVGTCRMLPSAFAEAGRTV 837
DB 777 LVLEIRQGFPTDTHLVKFTLYVGNWNKCDWVAIFLIVGTCRMLPSAFAEAGRTV 836
QY 838 LAMPDMVFTLRILHFAHKQLGPKIIIVVERMKDVPFFFLFSLVWLVAYGVTTQALLHP 897
DB 837 LAIDPMVFTLRILHFAHKQLGPKIIIVVERMKDVPFFFLFSLVWLVAYGVTTQALLHP 896
QY 898 HDGRLEWIFRRVLYRPLQIFQGLPDLDEIDARVNCSTHPLLEDSPSCPSLYANWL 957
DB 897 HDGRLEWIFRRVLYRPLQIFQGLPDLDEIDARVNCSTHPLLEDSPSCPSLYANWL 956
QY 958 LLVTELLVTNVLMLLIAMFSYTPQVQGNADMFQKQRYNLIYVYHERPALAPFILL 1017
DB 957 LLVTELLVTNVLMLLIAMFSYTPQVQGNADMFQKQRYNLIYVYHERPALAPFILL 1016
QY 1018 SHLSLTLRVFKKEAEKREHLERLDPDLPDQKVVTWQKFNFLSKMKERRRSEGEV 1077
DB 1017 SHLSLTLRVFKKEAEKREHLERLDPDLPDQKVVTWQKFNFLSKMKERRRSEGEV 1076
QY 1078 LRKTAHRVDIFAQYLGGLREKRIKLESQINYSVLVSSVADVLAQGG 1127
DB 1077 LRKTAHRVDIFAQYLGGLREKRIKLESQINYSVLVSSVADVLAQGG 1126

RESULT 6
Q9EPM3 PRELIMINARY; PRT; 1116 AA.
ID Q9EPM3;
AC Q9EPM3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ltrpc5 protein.
GN Name=Ltrpc5; Synonyms=Ltrpc5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129 SV;
RX PubMed=10915772; DOI=10.1093/hmg/9.12.1829;
RA Paulsen M., El-Maarri O., Engemann S., Stroedicke M., Franck O.,
RA Davies K., Reinhardt R., Reik W., Walter J.;
RT "Sequence conservation and variability of imprinting in the Beckwith-
RT Wiedemann syndrome gene cluster in human and mouse.";
RL Hum. Mol. Genet. 9:1829-1841(2000).
DR EMBL; AJ251835; CAC19457.1; -.
DR MGD; MGI:1861718; Trpm5.
GO; GO:0016021; C:integral to membrane; IEA.

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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuiura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaishizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasakawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi P., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK035197; BAC28976.1; -;
DR MGD; MG1:1861718; Trpm5.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005261; P: cation channel activity; IEA.
DR GO; GO:0004872; P: receptor activity; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrlP.
DR Pfam; PF00520; Ion trans_1.
DR PRINTS; PR01415; ANKRYIN.
KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
FT NON_TER 1
SQ SEQUENCE 1030 AA; 116983 MW; DDB31B7DF238F402 CRC64;

Query Match 73.3%; Score 4465.5; DB 2; Length 1030;
Best Local Similarity 84.4%; Pred. No. 5.8e-290;
Matches 858; Conservative 56; Mismatches 91; Indels 11; Gaps 3;

QY 151 LBEAQDFPVHPYEDDGGSGQLSDLSNLSHFILVEPFGKG-DGLTELRLLEKHS 209
DB 25 LSLAQEDTHIHPADEGNIQGPLCLDLSNLSHFILVESGALSGNDGLTELQSLLEKHS 84

QY 210 EQRAGYGGTGSIEIPVCLLVNGDPNTERISRAVEQAAPWLLVSGGIADVLALVNO 269
DB 85 QQRTGYGGTSCIPIVCLLVNGDPNTERISRAVEQAAPWLLVSGGIADVLALVNO 144

QY 270 PHLLVPKVAEKQPEKFPKSHSWEDIVRWTKLQNTISHLITVYDFEQSGSELDTV 329
DB 145 PHLLVPQVAEKQPEKFPKSHSWEDIVRWTKLQNTISHLITVYDFEQSGSELDTV 204

QY 330 ILKALVKACKSHQEQPDYLDLKLAVMDRVDIKSEIFNGDVWVKSCDLSEVMDALV 389
DB 205 ILKALVKACKSHQEQPDYLDLKLAVMDRVDIKSEIFNGDVWVKSCDLSEVMDALV 264

QY 390 SNKPEFVRLVFDNGADVADPLTYGRLOELVRSVRSKSLFLDLLQKQEAERLTLAGLGTQ 449
DB 265 SNKPDFVRLVFDNGADVADPLTYGRLOELVRSVRSKSLFLDLLQKQEAERLTLAGLGTQ 324

QY 450 QAREPPAGPAPFSLHVESRVKDFLODACHGFGYODGPGDRRAEKGAPKRPQKWLDD 509
DB 325 QARELPGLPAPFSLHVESRVKDFLODACHGFGYODGPGDRRAEKGAPKRPQKWLDD 380

QY 510 LNKSENPNPDLFLWAVLQNRHEMATYFWAMQEGVAAALAAKILKEMSHLSEAEAR 569
DB 381 LSRKSEDPWRDLFLWAVLQNRHEMATYFWAMQEGVAAALAAKILKEMSHLSEAEAR 440

QY 570 ATREAKYERLALDLFSECYSNSEARAFALLVRNRNCWKTTCCLHLATEADAKAFHAGCV 629
DB 441 TMREAKYEQLALDLFSECYNSNEDAFALLVRNRNHSRTTCLHLATEADAKAFHAGCV 500

QY 630 QAFUTRIWGDMAAGTPIILLGAFICPALVYNTLITFSEAPLRTGLEODLSDLDTE 689
DB 501 QAFUTKIWGDMAAGTPIILLGAFICPALVYNTLITFSEAPLRTGLEODLSDLDTE 560

QY 690 KSPLYGLQSVREIIVAEAPRAGQGRPRVALLTRKRFWAGAPVTVFLGNVVMYFAFLFLF 749
DB 561 KSFLCSRGGLQLEKTEAPRAPDGLGPOAFLITFRKRFWAGAPVTVFLGNVVMYFAFLFLF 620

QY 750 TYVLLVDFRPPPPQPGSPGVTLVFWFTLVLEETRQGFTEDETHLVKKFTLYVGDNNWK 809
DB 621 TYVLLVDFRPPPPQPGSPGVTLVFWFTLVLEETRQGFTEDETHLVKKFTLYVGDNNWK 680

QY 810 CDMAVAILFIVGVTCTRMPLPSAFAGRTVLAENDVFTLRLLHIFAIHKQLGPKIIVVERM 869
DB 681 CDMAVAILFIVGVTCTRMVPSVFEAGRTVLAIDFVFTLRLLHIFAIHKQLGPKIIVVERM 740

QY 870 MKDVFFFLFSLVWLVAYGVTTQALLPHDGRLEWIFRRVLYRYPYQIFGQIPDEIDEA 929
DB 741 MKDVFFFLFSLVWLVAYGVTTQALLPHDGRLEWIFRRVLYRYPYQIFGQIPDEIDEA 800

QY 930 RVNGSTHPLLEDSPSCPSLYANWLVLLVTFLLVNTNVLNLLIAMFSYTFQVQVQNA 989
DB 801 RVNCSLHPLLEDSSASCPNLVYANWLVLLVTFLLVNTNVLNLLIAMFSYTFQVQVQNA 860

QY 990 DMFWKFORYNLIVYHERPALAPPFILLSHLSLTLRRVFKKAEKRLHSLRDLPLDQ 1049
DB 861 DMFWKFORYNLIVYHGRPALAPPFILLSHLSLTLRRVFKKAEKRLHSLRDLPLDQ 920

QY 1050 KVTWETVQENFLSKMKRRRDSGEVLRKTAHRVDPIAKYVGLGRQEKRIKLESQI 1109
DB 921 KIITWETVQENFLSKMKRRRDSGEVLRKTAHRVDPIAKYVGLGRQEKRIKLESQI 980

QY 1110 NYCVSVLVSSVADVLAQGGGPRSSQCHGSGSLVLAADHRGGLDGMWEPQGPSPST 1165
DB 981 NYCMLLSSMTDTLAPGTYSSQNGCGRSQPASARDREYLE-----SGLPPSDT 1030

RESULT 8
QYTP4
ID Q7TFL4 PRELIMINARY; PRT; 1000 AA.
AC Q7TFL4;
DT 01-OCT-2003 (TREMREL. 25, Created)
DT 01-OCT-2003 (TREMREL. 25, Last sequence update)
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)
DE Transient receptor potential cation channel subfamily M member 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvxC57BL; TISSUE=Testis;
RC MEDLINE=12926392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
RA Hofmann T., Chubnov V., Gudermann T., Montell C.;
RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent
selective cation channel.";
RL Curr. Biol. 13:1153-1158(2003).
DR EMBL; AY280365; RAP44477.1; -;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005261; P: cation channel activity; IEA.
DR GO; GO:0004872; P: receptor activity; IEA.
DR GO; GO:0006812; P: cation transport; IEA.
DR InterPro; IPR002111; Cat channel_TrlP.
DR InterPro; IPR005821; Ion_trans.
KW Pfam; PF00520; Ion trans_1.
KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
SQ SEQUENCE 1000 AA; 112459 MW; BB107610176E6660 CRC64;

Query Match 71.5%; Score 4354.5; DB 2; Length 1000;
 Best Local Similarity 84.4%; Pred. No. 1.5e-282;
 Matches 842; Conservative 53; Mismatches 92; Indels 11; Gaps 4;

QY 1 MQDVQGRPGSGADREELGHRGVNFGSGKRGKFRVVPVSGVAPSVLFDLLASW 60
 DB 1 MQVTQSSCPGSPDTEGMEPILCRGEINFGSGKRGKFRVVPVSGVAPSVLFDLLASW 60
 QY 61 HLPAPNLVSLVGEOPFAMKSWLRLVRLKGLVKAQSTGAMLTLSALRVLARHVQAV 120
 DB 61 HLPAPNLVSLVGEOPFAMKSWLRLVRLKGLVKAQSTGAMLTLSALRVLARHVQAV 120
 QY 121 RDHSLASTKRVAVGASLGRVLRHRLLE--EAQEDFPVHYPPDDGSGSGLCSLDS 178
 DB 121 RDHSLASTKRVAVGASLGRVLRHRLLE--EAQEDFPVHYPPDDGSGSGLCSLDS 178
 QY 179 NLSHFVLVEPGPKG-DGLTEURLRLEKHSQAGYGGTGSIRIPVLCILVNGDPNTL 237
 DB 181 NLSHFVLVEPGPKG-DGLTEURLRLEKHSQAGYGGTGSIRIPVLCILVNGDPNTL 237
 QY 238 ERISRAVEQAAPWLLILVGGGIADVLAAVNPVPHLLVPKVAEKQKEKPPSKHFWEDIV 297
 DB 241 ERISRAVEQAAPWLLILVGGGIADVLAAVNPVPHLLVPKVAEKQKEKPPSKHFWEDIV 297
 QY 298 RWTLLQNTSHOHLTVYDFQSGSEELDTVLKALVKAQSHSQEPQDYDELKLAJA 357
 DB 301 HMTTELLQNTAAHPHLLTVYDFQSGSEELDTVLKALVKAQSHSQEPQDYDELKLAJA 357
 QY 358 WDRVDIAKSEIFNGDVWKSCLDEEVMDALVSNKPEFVRLVNDGADVAPLTYGRLOE 417
 DB 361 WDRVDIAKSEIFNGDVWKSCLDEEVMDALVSNKPEFVRLVNDGADVAPLTYGRLOE 417
 QY 418 LYRSVSRKSLDLQKQKQEAARLTAGLTQQAEPAGPAPFSLVSVRLKDFLQDA 477
 DB 421 LYRSVSRKSLDLQKQKQEAARLTAGLTQQAEPAGPAPFSLVSVRLKDFLQDA 477
 QY 478 CRGFYQDGPGRRAKGPAPKGTQKQWLLDLNOKSNPWRDLFLMAVLQNRHETATYF 537
 DB 481 CRGFYQDGPGRRAKGPAPKGTQKQWLLDLNOKSNPWRDLFLMAVLQNRHETATYF 537
 QY 538 WAMQGVGAALAAKILKEMSHLTAEAARATREAKYERLADLSECSYNSSEARAF 597
 DB 537 WAMQGVGAALAAKILKEMSHLTAEAARATREAKYERLADLSECSYNSSEARAF 597
 QY 598 LLVRNRCSWKTCLHLATEADAKAFFAHGQVQAFLTRIMWGMAGTPILRLLGATCP 657
 DB 597 LLVRNRCSWKTCLHLATEADAKAFFAHGQVQAFLTRIMWGMAGTPILRLLGATCP 657
 QY 658 ALVYTNLTIFSEAPLRTGLELDLSDTEKSPLYGLQSRVELVEAPRAQDGRPA 717
 DB 657 ALVYTNLTIFSEAPLRTGLELDLSDTEKSPLYGLQSRVELVEAPRAQDGRPA 717
 QY 718 VELLTRWRKFWGAPVTVLGNVVMYFAFLFTVTVLLVDRPPQSGPGRVTLVFWFT 777
 DB 717 VELLTRWRKFWGAPVTVLGNVVMYFAFLFTVTVLLVDRPPQSGPGRVTLVFWFT 777
 QY 778 LVLEIRQGFDETHLVKFTLVYVGNWKNKDMVAIFLFIIVGVTCTMLPFAEAGRTV 837
 DB 777 LVLEIRQGFDETHLVKFTLVYVGNWKNKDMVAIFLFIIVGVTCTMLPFAEAGRTV 837
 QY 838 LAMDFWFTLRIHFAHKGKPKIIVVERWMDKVFLLFLLSVMLVAVGVTTQALLHP 897
 DB 837 LAMDFWFTLRIHFAHKGKPKIIVVERWMDKVFLLFLLSVMLVAVGVTTQALLHP 897
 QY 898 HDGRLEWTFRVLVRYPIQFQIPLDEIDEARVNCSTHPLLEDSPSCSLYANMLVIL 957
 DB 897 HDGRLEWTFRVLVRYPIQFQIPLDEIDEARVNCSTHPLLEDSPSCSLYANMLVIL 957
 QY 958 LLVTFLLVTVNLLNMLIAMSYFQVVOGNADFWKFP 995
 DB 957 LLVTFLLVTVNLLNMLIAMSYFQVVOGNADFWKFP 995

RESULT 9
 Q8TD43
 ID Q8TD43 PRELIMINARY; PRT; 1214 AA.
 AC Q8TD43;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cation channel TRPM4B (Transient receptor potential ion channel melastatin subgroup member 4 protein) (Transient receptor potential cation channel subfamily M member 4 splice variant B).
 GN Name=TRPM4B; Synonyms=TRPM4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22011788; PubMed=12015988; DOI=10.1016/S0092-8674(02)00719-5; Launay P., Fleig A., Ferraud A.L., Scharenberg A.M., Penner R., Kinet J.P.;
 RA "TRPM4 is a Ca2+-activated nonselective cation channel mediating cell membrane depolarization.";
 RT Cell 109:397-407(2002).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX Perraud A.-L., Scharenberg A.;
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Prostate;
 RA MEDLINE=22791733; PubMed=12799367; DOI=10.1074/jbc.M305127200; Nilius B., Prenen J., Droogmans G., Voets T., Vennekens R., Freichel M., Wissenbach U., Flockerzi V.;
 RA "Voltage dependence of the Ca2+ activated cation channel TRPM4.";
 RT J. Biol. Chem. 278:30813-30820(2003).
 RL [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7; Hofmann T., Chubakov V., Gudermann T., Montell C.;
 RA "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent selective cation channel.";
 RT Curr. Biol. 13:1153-1158(2003).
 DR EMBL; AF497623; AAM18083.1; -;
 DR EMBL; AJ575813; CAE05941.1; -;
 DR EMBL; AY297045; BAP44474.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002111; Cat channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Iontrans; 1.
 DR Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
 SQ SEQUENCE 1214 AA; 134300 MW; 76ADA452690ED8F5 CRC64;
 Query Match 40.2%; Score 2448.5; DB 2; Length 1214;
 Best Local Similarity 45.6%; Pred. No. 9.2e-155;
 Matches 534; Conservative 177; Mismatches 350; Indels 111; Gaps 26;
 QY 26 GEVNFSGSKKRGKFRVVPVSGVAPSVLFDLLAEHMLPAPNLVSLVGEOPFAMKSWLR 85
 DB 76 GELDTGAGRKHSNRLSLDRTPAATVSLVTRTWGFRAPNLVSVLGGSPVLTWLQ 135
 QY 86 DVLRLKGLVKAQSTGAMLTLSALRVLARHVQAVRDHSLASTSTKRVAVGASLGRV 145
 DB 136 DLRLRGLVKAQSTGAMLTLSALRVLARHVQAVRDHSLASTSTKRVAVGASLGRV 194
 QY 146 LHRRLILEAQEDFPVHY-----PEDDGSQGLCSLDSNLGSHFIIIVPEGPKGDLTEL 200
 DB 195 RNRDTLNPKGSPFARYRWGRDPP--GVQFP---LDYNSAFFLVDGTHGCLGENRF 249
 QY 201 RLRLKHLSEQAQGGTGSIEIPLVLCILVNGDPNTLERISRAVEQAAPWLLVSGSGIA 260

Db 250 RLRLSYISQKTVGGTG-IDIPVLLLLIDGDEKMLTRIENATQAOLPCLLVAGSGAA 308
 Qy 261 DVLAALVNQPHLLVP-----KVAEKQKPKSPKSHSWEDIVRWTKLLQNTSHQHL 313
 Db 309 DCLATLEBD--TLAPGSGGARGEARDIRFFPK-----GDLEVLQAOVERIMTRKELL 361
 Qy 314 TVYDFEQSSELDTVILKALVKACKSHSQPDYLDLKLAVADRWVDIAKSHIFNGDV 373
 Db 362 TVYSSE-DGSEFEFIVLALVKAC--GSSEASAYLDELAVANRWVDIAQSELFRGDI 418
 Qy 374 EWKSCDLEVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYSRVSRLKLLFDLQ 433
 Db 419 QWRSHLEASLMDALLNDRPEFVRLLSHGLSLGHFLTPMLAQLYSAAPNSLIRNLLD 478
 Qy 434 RKQEARLTLAGL--GTQOAREPPAGPAPFSLHEVSRVLKDFLODACRGFFQDGRPD 491
 Db 479 QASHSAGTKAPALKGAALRPP-----DVGHVRLMLLGMKCAAPRYPGSGAWDPH 528
 Qy 492 RAEGKPAKRPCTQKWLIDLNQK-----ENPWRDLFWAVLQNRHEMATYFWAMQ 542
 Db 529 -----PGGFGESWYLLSDKATSPSLDAGLQOAPWSDLLWALLNRAQWYFWENG 583
 Qy 543 EGVAALAAKILKEMSHLEAEAAARATREA--KYERLALDLPSECYSNSEARAFALLV 600
 Db 584 NAVSSALGACLLLRVWARLEPDAEAAARRKDLAFKFGVDFLFCGYRSEVRAARLL 643
 Qy 601 RNRCSWKTTCUHLATEADAKAFFAHGVOAELTRIMWDMAGTPLLRLGALCPALV 660
 Db 644 RRCPLMGATCQLQAMQADARAFFAQDGVQSLTQKMGDMASTTPIWALVLAFFCPPLI 703
 Qy 661 YTNLITF--SEAPLRTGLDQLDLSLDTKSPLYGLQSRVEELVEAPRAQGD----- 712
 Db 704 YTRLITFRKSEPTREELE--FDMDSVINGSGPVTADPAKTPGLVPRQSGRPGCCGG 761
 Qy 713 --RGPRAVPLLRKFWGAPVTVFLGNVVMYFAFLFVYLLVDVFRPPPGSGPEVT 770
 Db 762 RCGGRC---LRWFHFWGAPVTIFMGNVSYLLFLLFSRVLVDFQAP--PGSLELL 816
 Qy 771 LYFWFTLVLEIRQGFTEDET-----HLVKKFTLYVGNWKNKCDMVALFLFI 819
 Db 817 LYFWAFTLLCELRQGLSGGGLASGGPGGHASLSQRRLYLADSMNQCIDLVALTCFL 876
 Qy 820 VGVTCMLPSAEAGRTVLAMPVFTLRLHFAHKGOLGPKIIVVERMKDVPFFLFF 879
 Db 877 LGVGCKLTPLGLHLGRTVLICIDFMVFTVRLHLHFTVKNKGPKIVIVSKMKDVFLEFF 936
 Qy 880 LSVLVAVGYTTQALHPHGRLEWIFRRVLYRPLQIFQIPLDIBEARV---NCSTH 936
 Db 937 LGVWLAVGYATEGLLRPRDSPPSILRRVYRPLQIFQIPEQDMVALMEHNSCSSE 996
 Qy 937 PLLLEDSP-----SCPSLVANMLVILLVTFLLVTVNLLMULLIAMFSTTFQVQGNAM 991
 Db 997 PGWAHPPGAQAGTCVSYQVANLVLLVILLVILVANILLVLLIAMFSTTFQVQGNADL 1056
 Qy 992 FKKFQRYNLIVEHSPALAPPILLSHLSLTLRRVFKK-----EAEKREHLERD 1042
 Db 1057 YKKAQRYLRTREPHSRPALAPPVIVISHLRLRLLCRRPRSPQSPALHPRVYLSKE 1116
 Qy 1043 LPDPLQKQVVTWETQKENPLSKWEKRRDSEGEVLRKTAHRVDFIAKYLGLRQEOKRI 1102
 Db 1117 -----AERKLLTWESVHKNFLLARADKRESDSERLKRTSQKVDLALKQLGHIREYEQRL 1172
 Qy 1103 KCLESQINYSVLVSSVADVLAQG-----GGP 1129
 Db 1173 KVLEREVQCSRVLGWVAEALSRSALIPGCGP 1204

RESULT 10

Q7TN37

PRELIMINARY; PRT; 1213 AA.

AC Q7TN37

01-OCT-2003 (T-REMBurel. 25, Created)

DT 01-OCT-2003 (T-REMBurel. 25, Last sequence update)

DT 01-MAR-2004 (T-REMBurel. 26, Last annotation update)
 DE Transient receptor potential ion channel melastatin subgroup member 4
 DE protein.
 GN Name=trpm4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=SVJ129; TISSUE=Heart;
 RX MEDLINE=22791733; PubMed=12799367; DOI=10.1074/jbc.M305127200;
 RA Nilius B., Prenen J., Droogmans G., Voets T., Vennkens R.,
 RA Feichel M., Wissenbach U., Flockerzi V.;
 RT "Voltage dependence of the Ca²⁺ activated cation channel TRPM4.";
 EL J. Biol. Chem. 278:30813-30820(2003).
 DR EMBL; AJ575814; CA805940.1;
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0005262; F:calcium channel activity; IDA.
 DR GO; GO:0006816; P:calcium ion transport; IDA.
 DR InterPro; IPR002111; Cat channel_TripL.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Ion_trans; 1.
 KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
 SQ SEQUENCE 1213 AA; 135759 MW; E4959F53ED35FB66 CRC64;

Query Match 39.4%; Score 2399.5; DB 2; Length 1213;

Best Local Similarity 43.6%; Pred. No. 1.8e-151;

Matches 530; Conservative 185; Mismatches 343; Indels 157; Gaps 30;

Qy 26 GEVNFSGSKGRKFRVPSVGVAPSVLFDLLAEHLAPNLVSLVSGEOPFAMKSWLR 85
 Db 77 GDLDFTYSGRHSNFLRLSDRTDPATVYSLVTSWGFAPNLVSVLGGSGPVLQTLQ 136
 Qy 86 DVLKGLVKAAQSTGAWLTSLARVGLARHVGQAVRDHSLASTSTKRVAVVAGMASLGRV 145
 Db 137 DLLRRGLVRAAQSTGAWITVGTGLHTGIGHRVGAVRDHQTASTGSS--KVAMGVAPWGV 195
 Qy 146 LHRRLLEAQQEDFPVHY-----PEDDGGSGPLCSLDLSNLHFLVPEGPGKGDGLTEL 200
 Db 196 RNRDMLNPKGSPFARYRWGDPED--GVPEP---LDYNSAFFLVDDGTGRGNGENRF 250
 Qy 201 RLRLKHLISEORAGYGGTGSIEIPVCLLVNGDPNTERISRAVQAAAPWLILVSGGIA 260
 Db 251 RLRFESYVAQKTGVGGTG-IDIPVLLLLIDGDERMLKRIEDATQALPCLLVAGSGAA 309
 Qy 261 DVLAALVNQPHLLVP-----KVAEKQKPKSPKSHSWEDIVRWTKLLQNTSHQHL 313
 Db 310 DCLVETLED--TLAPGSGGLRRGEARDIRRYFPK-----GDPEVLQAOVERIMTRKELL 362
 Qy 314 TVYDFEQSSELDTVILKALVKACKSHSQPDYLDLKLAVADRWVDIAKSHIFNGDV 373
 Db 363 TVYSSE-DGSEFEFIVLALVKAC--GSSEASAYLDELAVANRWVDIAQSELFRGDI 419
 Qy 374 EWKSCDLEVMVDALVSNKPEFVRLFDVNGADVADFLTYGRLOELYSRVSRLKLLFDLQ 433
 Db 420 QWRSHLEASLMDALLNDRPEFVRLLSHGLSLGHFLTPMLAQLYSAVSPNSLIRNLLD 479
 Qy 434 RKQEARLTLAGLGTQOAREPPAG-----PPAFSLHEVSRVLKDFLODACRGFY----- 482
 Db 480 QASH-----ASSKSPPVNGTVELRPP-----NVGQVRLTLGLTCAPRYPART 524
 Qy 483 -----QDGRPGDRRAEKGPAPKPTGQKWLIDLNQK-----SENWRDLFWAVLQ 528
 Db 525 RDSYLQDQDREND-----SLMDMANKQPSDASFEQAPWSDLLIALLL 569
 Qy 529 NRHEMATYFWAMQEGVAAALAAKILKEMSHLEAEAAARATRE--AKYERLALDFSE 586
 Db 570 NQAQWAIYFWEGKSNVSALGACLLLRVWARLESEAEAEAAARRKDLAATFESMVDLFCG 629
 Qy 587 CYSNSEARAFALLVRRNRCSWKTTCUHLATEADAKAFFAHGVOAELTRIMWDMAGT 646

Db 630 CYHNSERAARLLRRCLPWGEATCLQAMQADARAFPAQGVQSLTQKWMGEMDSTTP 689
 QY 647 ILRLGAFCLCPALVYNTLTP--SEAPRLTGLDQLDLSLDTKSPGLYQKVEELV 704
 Db 690 IYALLAFPCPLLYTNLIVFRKSEETQKLD--FDMSSINGAGPGGIVESAVAL 747
 QY 705 EAPRAQDGRPRAVE--LLTWKRFWGPATVFLGNVVMYFAFLFTYVLLVDFRPPP 761
 Db 748 E--RRQRPRGALCCGFKSKWDFWGPATVFLGNVVMYFAFLFTYVLLVDFRPPP 805
 QY 762 QGPSGEVLYPWVTLVLEIRQGF-----FTDEDTHLVKFKTLYVGDNNKC 810
 Db 806 --PSVELLYFWAFTLLCELRQGLGGWGLASGGGPDRAPLRHLHLVLSDTWQC 863
 QY 811 DNVAIFLFLVGVTCRMLPSAFEGRTVLAMDPMVFTLRLHI FAIHKQLGPKIIVVERMM 870
 Db 864 DLLALTCLLGVGCLTGLDGLRTVLCDFMTFTLLHIFTVNLQKLPKIVIVSKM 923
 QY 871 KDVFLLFLLSVLVAVGVTTQALLHPHGDGRLEWIFRVLRYPLQIFGOIPLDEIDAR 930
 Db 924 KDVFLLFLLSVLVAVGVATEGILRPQDRSLPSILRVRVYPLQIFGOIPQEMDVAL 983
 QY 931 V---NCS-----THELLEDSP---SCPSLYANWLVILLVTLVTLVTLVLLNLIAMF 978
 Db 984 MIPGNCSEWERSWHP-----EGPVAGSCVQYANWLVLLVILLVTLVTLVLLNLIAMF 1039
 QY 979 SYTFQVQGNADMFQPKQRYNLIVYHERPALAPPFTLLSHLSLTLR-----RVFKK 1030
 Db 1040 SYTFQVQGNADMFQPKQRYNLIVYHERPALAPPFTLLSHLSLTLR-----RVFKK 1030
 QY 1031 EAEKREHLERDLPDLDQKVVTVQKFNFLSKWKKRRRDSGEVLAKTAHRVDIAK 1099
 Db 1100 PASPVFHFVCLSKAEARLLTWESVHKENFLLAQAKRDSRLKRTSKQVDITAL 1159
 QY 1091 YLGLREKREIKLESQINQSVLVSSVADVLAQGGPRSSQHCQSGSOLVAADHRGL 1150
 Db 1160 QLGQIREYDRRLGLEREVQCHSRVLTWAEALSH-----SALL----- 1198
 QY 1151 DGWEQPCAGPPSDT 1165
 Db 1199 -----PPGAPPPSPSPT 1209

RESULT 11
 Q96L84 ID Q96L84 PRELIMINARY; PRT; 1040 AA.
 AC Q96L84;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE TRP-related cation influx channel (Transient receptor potential cation channel subfamily M member 4 splice variant A).
 GN Name:TRPM4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21438010; PubMed=11535825; DOI=10.1073/pnas.191360198;
 RA Xu X.-Z., Moebius F., Gill D.L., Montell C.;
 RT "Regulation of melastatin, a TRP-related protein, through interaction with a cytoplasmic isoform";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:10692-10697 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Xu X.-Z., Moebius F., Gill D.L., Montell C.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
 RA Hofmann T., Chubakov V., Gudermann T., Montell C.;
 RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent

selective cation channel.";
 RT Curr. Biol. 13:1153-1158 (2003).
 DR EMBL; AY046396; AAL02142.1; -;
 DR EMBL; AY297044; AAP44473.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Ion_trans; 1.
 KW Ion transport; Ionic channel; Receptor; Transmembrane; Transport.
 SQ SEQUENCE 1040 AA; 115564 MW; 684A8C554B2B0F2E CRC64;

Query Match 35.9%; Score 2184.5; DB 2; Length 1040;
 Best Local Similarity 45.3%; Pred. No. 3.5e-137;
 Matches 486; Conservative 156; Mismatches 320; Indels 111; Gaps 26;

QY 125 LASTSTKRVVAVGMSLGRVLRHRLLEEAQEPFVHY-----PEDDGGSGQLCSLDN 179
 Db 1 MASTG-GTKVAVGVAWGVVRNRTLINPKGFPARYWRGDPED--GVQPP--LDYN 54
 QY 180 LSHFLLVPEPPGKGDGLTBLRLRLEKHISEQAGYGGTGSIEIPVLCVLLVNGDPMTLR 239
 Db 55 YSAFFLVDDGTHGCLGSENRFRRLRESYISQQTGVGGTG-IDIPVLLLLIDGDEKMLTR 113
 QY 240 ISRAVEQAAPWLILVSGGGIADVLALVNQPHLLVP-----KVAKQFKEKFPKXHS 292
 Db 114 IENATQALPCLLVAGSGGADCLAELED--TLAPGGGARGQGEARDRIREFPK-- 167
 QY 293 WEDIVWTKLLQNTSHQHLTYDPEQSGSELDITVLKLVKACKSHSQSPQDYLDEL 352
 Db 168 -GDEVLQAVQVERIMTKELLTVYSSE-DGSEEFETVLKLVKAC--GSSASAYLDEL 223
 QY 353 KLAVANDRVDIKSEIFNGDVKNKCDLEVMVDALVNKPEFVRLFVNDGADVDFLT 412
 Db 224 RLAVANVRVDIAQSELFRGDIQWRSFHLSEALMDALLNDRPEFVRLLSHGLSHGLFLTP 283
 QY 413 GRLQELYSRSKSLFLDILLQKQBEARLTLAGL--GTQOAREPPAGPAPSLHEVSEVL 470
 Db 284 MRLAQLYSAAPSNSLIRNLLDQASHAGTKAPALKGGAAELRP-----DVGHVL 333
 QY 471 KDFLODACHGFYDGRPDGRRAEKGPAKRPFGKWLLDLNQK-----ENPWRDL 521
 Db 334 RMLLGKMCAPYPSGGAWDPH-----PQGGFESNYLLSDKATPSLSDAGLGQAPMSDL 388
 QY 522 FLWAVLQNRHEMATYFWAMGQGVAAALAAACKILKEMSHLETEAARATREA--KYERL 579
 Db 389 LLWALLLNRAQWAMYFWEGSNVSSALGACLLRVMARLEPDAEAAARKDLAFKPEGM 448
 QY 580 ALDLSECYSSSEARAPALIVRRNRCSKTTCLHLATEADAKAFPAHDGVQAFTRIWWG 639
 Db 449 GVDLGECTRSSEVRAARLLRRCPLMGDATCLQAMQADARAPFAQGVQSLLTQKWWG 508
 QY 640 DMAAGTPIRLILGALPCPALVYTNLITF--SEAPRLTGLDQLDLSLDTKSPGLYGLQ 697
 Db 509 DWASTTPIWALVLAFFCFPLIYTLITFRKSEEBPTREELE--FDMDSVINGPVGVTAD 566
 QY 698 SRVLEVEAPRAQGD-----RGPRAVFLTLTRKRWKPGAPVTVFLGNVVMYFAFLFLF 749
 Db 567 PAEKTPGLGVPRQSGRPGCCGRCGRRC---LRWFHFWGAPVTIFMGNVSVLLFLFLF 623
 QY 750 TYVLLVDFRPPPPQSGPVEVTLVFWVTLVLEIRIQGFTDEDT-----HLVKK 798
 Db 624 SRVLLVDFQAP--PGSLELLYFWAFTLLCELRQGLSGGSGGLASGGPGPGHLSOR 681
 QY 799 FTLVYGNWKNCKMVAIFLVGVTCRMLPSAFEGRTVLAMDPMVFTLRLHI FAIHKQ 858
 Db 682 LRLYLADSWNQCDLVALTCFLGVLGVCRLTGLVHLGRTVLCIDFMVFTVLLHIFVNLQ 741
 QY 859 LGPKIIVVEENMKDVFFFLFFFLSVLVAVGVTTQALLHPHGDGRLEWIFRVLRYPLQIF 918
 Db 742 LGPKIIVISKMKDVFFFLFFFLGVMLVAVGVATEGILRLRPRDSDFPSILRVRVRYPLQIF 801

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Qy 919 GOIPLEIDEARV---NCSTHPLLEDSP-----SCPSLYANWLVILLVTLVTLVTVLL 970
Db 802 GOIQEDMDVMEHNSCSSEPGFWAHPPGAAGTCVSOYANWLVLLVTLVTLVTVLL 861
Qy 971 NLLIAMFSYTFQVVOGNADMFQRYNLIYVHERPALAPPFILLSHLSLTIRRVFKK 1030
Db 862 VNLIIAMFSYTFQVVOGNADMFQRYNLIYVHERPALAPPFILLSHLSLTIRRVFKK 921
Qy 1031 -----EAPHKEHLERDLPDLDOKVTVTWQENFLSKMEKRRRDEGEVLKRT 1081
Db 922 PRSPQSSPALEHFRVYLSKE-----AERKLLTWESVHKENFLARADKRESDSERLRT 977
Qy 1082 AHRVDPIAKYLGGLREQEKRIKLESQINYSVADVLAQG-----GSP 1129
Db 978 SOKVDLALKQLGHIREYEQRLKVLREVOQCVRVLGWAEALSRSALLPPGSP 1030

RESULT 12
Q9NXV1 PRELIMINARY; PRT; 1016 AA.
AC Q9NXV1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ20041.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isoqai T., Sugano S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000048; BAA09097.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR Pfam; PF00520; Ion trans; 1.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW ION TRANSPORT; IONIC CHANNEL; TRANSMEMBRANE; TRANSPORT.
SQ SEQUENCE 1016 AA; 113245 MW; F640689A3D94DC6D CRC64;

Query Match 35.5%; Score 2164; DB 2; Length 1016;
Best Local Similarity 45.6%; Pred. No. 8.1e-136;
Matches 480; Conservative 150; Mismatches 316; Indels 106; Gaps 25;

Qy 125 LASTSTKRVVAVGMASLGRVLRHRLRILEAQEDFPVHY-----PEDDGSQGPLCSLDN 179
Db 1 MASTG-GTKVAVGAPWGVNRDRLINPKGSFPARYRWGDPED--GVQFP---LDYN 54
Qy 180 LSHFIVGPPGKDGGLTELRLRLRLEKHSIQAGYGGTSGEIPVLCILVNGDPNLTIR 239
Db 55 YSAFFLVDDGTHCLGGENRFRRLRLESYSQQKTGVGGTG-IDIPVLLLLIDGDEKMLTR 113
Qy 240 ISRAVEQAAPWLLVSGGGIADVLALVNQPHLLVP-----KVAEKQFKKFPKSHFS 292
Db 114 IENATQAPCLLVAGSGGAUCLAEITLED--TLAPGSGARGEARDRIRFFPK----- 167
Qy 293 WEDIVRWTKLLQNITSHOHLITVYDFEQEGSEELDTVLKALVKACKSHSQEPQDYDEL 352
Db 168 -GDLEVLQAVQERIMTRKELLTVYSSE-DGSEEFETIVLKALVKAC--GSSEASAVLDEL 223
Qy 353 KLAVANDRVIAKSEIFNGDVHKSQDLBEMVDALVSNKPEFVRLPVDNGADVADFLTY 412
Db 224 RLAVANRVDAIQSEIFNGDVHKSQDLBEMVDALVSNKPEFVRLPVDNGADVADFLTY 283
Qy 413 GRLOELYSRSKLLFDLLQKQEBEARLTLAGI--GTQQAEREPPAPPAFSLHSEYRVL 470
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Db 284 MRLAQLYSAAPSNSLIRNLLDQASHAGTAPKAPALKGGAAELRPP-----DVGHVL 333
Qy 471 KDFLODACRFYQDGRPGDRRAEKGPAPKPTGQKWLLDLNQKS-----ENPRDL 521
Db 334 RMLLGKWCAPRYPSGGAWDPH-----PGQGFGEWYLLSDKATSPSLDAGLQAPWSDL 388
Qy 522 FLNAVLONRHEMATYFWAMQOEGVAAALAAACKILKENSHELETEAARATREA--KYERL 579
Db 389 LLWALLINRAQMAFYFWEMGSNAVSSALGACLLLRVVMARLEPDAEAAARAKDLAFKPEGM 448
Qy 580 ALDLPFSECYNSSEARAFALLVRNRNCWSKTTCLHLATEADAKAPFAHFDGVOAFTRIIWWG 639
Db 449 GVDLFGECYSESEVRAARLLRRCPMGDATCLQANQADARAFQAQGVQSLITQKWWG 508
Qy 640 DMAAGTPIRLILGAFALPVTNLTTF--SEEAPLRTGLDQLDLSLDTESPLVGLQ 697
Db 509 DMASTTPIWALVLAFFCPPLIYTRLIITFRKSEBETREELE--FDMDSVINGECPVGTD 566
Qy 698 SRVEELVEAPRAQD-----RGPRAVFLLTWRFKFWGAPVTVFLGNVVMYFAFLFLF 749
Db 567 PAEKTPLGVPRQGRPGCGGRCGRRC---LREWFHFWGAPVTTFMGNVVSYLLFLLLF 623
Qy 750 TYVLVDPRPPQSGPEVTLYFVFTLVLEETIRQGFETDDEDT-----HLVKK 798
Db 624 SRVLLVDFQAPAP--PGSLELLLYFWAFTLLCEEURLQGLSGGGSLASGPGPGHASLSQR 681
Qy 799 FTLVGNWNKCDMVAIFLFIYGVTCRMLPSAFAGRTVLAMDPMVFTLRLIHIPAIHKQ 858
Db 682 LRLVLAWSNQCDLVALTCFLGVCRLTPGLYHLGRVLCIDFMVFTVRLHLHIFTVNKQ 741
Qy 859 LGPKIIVVERMMKDVFFFLFPLSVLWVAYGVTQALLPHDGRLEWIFRRVLYRPLQIF 918
Db 742 LGPKIIVSVKMKDVFFFLFPLSVLWVAYGVTQALLPHDGRLEWIFRRVLYRPLQIF 801
Qy 919 GOIPLEIDEARV---NCSTHPLLEDSP-----SCPSLYANWLVILLVTLVTLVTVLL 970
Db 802 GOIQEDMDVMEHNSCSSEPGFWAHPPGAAGTCVSOYANWLVLLVTLVTLVTVLL 861
Qy 971 NLLIAMFSYTFQVVOGNADMFQRYNLIYVHERPALAPPFILLSHLSLTIRRVFKK 1030
Db 862 VNLIIAMFSYTFQVVOGNADMFQRYNLIYVHERPALAPPFILLSHLSLTIRRVFKK 921
Qy 1031 -----EAPHKEHLERDLPDLDOKVTVTWQENFLSKMEKRRRDEGEVLKRT 1081
Db 922 PRSPQSSPALEHFRVYLSKE-----AERKLLTWESVHKENFLARADKRESDSERLRT 977
Qy 1082 AHRVDPIAKYLGGLREQEKRIKLESQINYS 1113
Db 978 SOKVDLALKQLGHIREYEQRLKVLREVOQCQS 1009

RESULT 13
Q7Z5D9 PRELIMINARY; PRT; 1069 AA.
AC Q7Z5D9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transient receptor potential cation channel subfamily M member 4 splice variant C.
GN Name=TRPM4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22726392; PubMed=12842017; DOI=10.1016/S0960-9822(03)00431-7;
RA Hofmann T., Chubakov V., Gudermann T., Montell C.;
RT "TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent selective cation channel."
RL Curr. Biol. 13:1153-1158(2003).
RL EMBL; AY297046; AAP44475.1; -.
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RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK044094; BAC31771.1;
DR MGD; MGI:1915917; Trpm4.
DR GO; GO:0016021; C.integral to membrane; TAS.
DR GO; GO:0005886; C.plasma membrane; IDA.
DR GO; GO:0005262; F.calcium channel activity; IDA.
DR GO; GO:0006816; P.calcium ion transport; IDA.
DR InterPro; IPR002111; Cat channel_Trlp.
DR InterPro; IPR005821; Ion trans.
DR Pfam; PF00520; Ion trans_1.
DR Ion transport; Ion channel; Transmembrane; Transport.
KW SEQUENCE 945 AA; 105526 MW; B7261COA36866EB CRC64;
SQ

Query Match 34.0%; Score 2069; DB 2; Length 945;
Best Local Similarity 45.8%; Pred. No. 1.7e-129;
Matches 455; Conservative 141; Mismatches 124; Indels 27;

QY 100 GAWILTSALRVGLRHVGQVRDHSLASTSTKRVVAVGMSLGRVLRHLEAEQEDPP 159
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 GAWIVTGGTGTGIRHVGVAVRDQSTGSS-KVAVGVAPMGVVRNDRMLNPKGSPF 62

QY 160 VHY-----PEDDGGSGCLSDNSLHPTLVPBPFGDGTLELRLEKHISQKAG 214
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 ARYWRGDPED--GVEFP---LDYNISAPFLVDGTYGRLGGRNRRFLRFESVAAQKYG 117

QY 215 YGCTGTEIPVCLLVNGDPTLIERISRAVEQAPWLLLVGSGGIADVLAAVNPQHLV 274
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
118 VGGTG-IDIPVLLLLIDGDEKMLKRIEDATQAQLPCLLVAGSGGAADCLVETLED--TLA 174

QY 275 P-----KVAEQKFKPKSPKSPFSDIVRWTKLLQNTSHOHLITVYDFEGSGEELD 327
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
175 PGSGGLRRGEARDIRRYFPK-----GDPEVLAQVVERIMTRKELLTVYSSE-DGSEEF 228

QY 328 TVTLKALVACKSHSOPQDYLDELKIAVADRDVIAKSIIFNGDEWKSCLDEEVVWDA 387
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
229 TIVRLALVKAC--GSSASAYLDELRLAVANRNDIAQSELFRGDIQWRSFHLEASLMDA 286

QY 388 LVSNKPEFVRLVDNGADVADFTYGRLOELYSRVSRSKSLLPDLQKQBEARLTLAGLG 447
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
287 LINDREFVRLLSHGLSLGHFTPVRLAQLYSAVNSPNSLIRNLLDQASH----- 336

QY 448 TQQAAREPPAG-----PPAFSLHEVSRVSKDFLQDACRGY-----QDGPGR 490
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
337 ASSSKSPVNGTVELRPP-----NVGQVRLTLGGETCAPRYPARNTRDSYLGQDHREND- 390

QY 491 RRAEKGAKPTGCKWLLLDLNQK-----SENPRDLFLAVLQNRHEMAYFWAMGQ 542
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
391 -----SLMDWANKQKPTDSTAFEQAPQSDLLIALLNRAQMAIFYWFKSGS 436

QY 543 EGVAALAAACKILKEMSHLETAEAARATRE--AKYERLALDLFSECYSNSEARAFALLV 600
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
437 NSVASALGACLLLRVMALESEAEARRKDLATFESMSVDLFGECYHNSSEARAELLL 496

RESULT 15
TRL2 HUMAN
ID TRL2 HUMAN STANDARD; PRT; 1503 AA.
AC O94759; Q96KNG;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Long transient receptor potential channel 2 (LTPC2) (Transient
DE receptor potential channel 7) (TRPC7).
GN Name=TRPM2; Synonyms=KNP3, LTRPC2, TRPC7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99026133; PubMed=9806837; DOI=10.1006/geno.1998.5551;
RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Asakawa S., Ito F.,
RA Shimizu N.;
RT "Molecular cloning of a novel putative Ca2+ channel protein (TRPC7)
RT highly expressed in brain";
RL Genomics 54:124-131(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX PubMed=11960981; DOI=10.1074/jbc.M112096200;
RA Wehage E., Eisfeld J., Heiner I., Jungling E., Zitt C., Luckhoff A.;
RT "Activation of the cation channel long transient receptor potential
RT channel 2 (LTPC2) by hydrogen peroxide. A splice variant reveals a
RT mode of activation independent of ADP-ribose";
RL J. Biol. Chem. 277:23150-23156(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Tokitani Y., Choi D.-K., Soeda S.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,

Db 1137 QFQKQREPEQKIEDISNKVDAMVDLDDPLKRSISM--EORLASLEEQVAQTARALHW 1193
Qy 1119 VADVLAQGGPRSSQHCSEGSOLVAAD---HRGGLDGHEQPG 1157
Db 1194 IVRTLRSAGFSSEADVPTLASQKAAEEPDPEFGRKKTEEPG 1235

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